

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:21:11 ; Search time 60 seconds
(without alignments)
7666.919 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgccggtggcgag.....tgacggaggttaaccagtga 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246	16.4	2880	1	US-08-462-484-3
2	246	16.4	2880	1	US-08-441-147-3
3	246	16.4	2880	5	PCT-US95-07536-3
4	38	2.5	2418	1	US-08-462-484-1
5	38	2.5	2418	1	US-08-441-147-1
6	38	2.5	2418	5	PCT-US95-07536-1
7	35	2.3	2925	1	US-08-462-484-9
8	35	2.3	2925	1	US-08-441-147-9
9	35	2.3	2925	5	PCT-US95-07536-9
10	30	2.0	2860	1	US-08-462-484-7
11	30	2.0	2860	1	US-08-441-147-7
12	30	2.0	2860	5	PCT-US95-07536-7
13	24	1.6	3102	1	US-08-462-484-5
14	24	1.6	3102	1	US-08-441-147-5
15	24	1.6	3102	5	PCT-US95-07536-5
16	21	1.4	1161	3	US-08-689-421-22
17	21	1.4	1161	4	US-09-389-528-22
18	21	1.4	1161	4	US-09-181-827A-22
19	21	1.4	2940	3	US-08-689-421-28
20	21	1.4	2940	4	US-09-389-528-28
21	21	1.4	2940	4	US-09-181-827A-28
22	20	1.3	533	4	US-09-198-119C-66
23	20	1.3	768	4	US-09-198-119C-66
24	19	1.3	1088	3	US-09-040-285A-1
25	19	1.3	2009	1	US-07-958-222A-1
26	18	1.2	1155	4	US-08-818-112-12
27	18	1.2	1155	4	US-08-818-111-12

28	18	1.2	1155	4	US-09-056-556-12	Sequence 12, Appl
29	18	1.2	1155	4	US-09-072-596-12	Sequence 12, Appl
30	18	1.2	2574	4	US-09-255-829-27	Sequence 27, Appl
31	17	1.1	17	1	US-08-526-964-6	Sequence 6, Appl
32	17	1.1	17	2	US-08-946-617-6	Sequence 6, Appl
33	17	1.1	17	4	US-09-080-625-16	Sequence 16, Appl
34	17	1.1	17	4	US-09-695-782-16	Sequence 16, Appl
35	17	1.1	18	4	US-08-898-180-15	Sequence 15, Appl
36	17	1.1	19	4	US-09-115-475-4	Sequence 4, Appl
37	17	1.1	20	3	US-08-750-145A-12	Sequence 12, Appl
38	17	1.1	20	3	US-08-975-698A-9	Sequence 9, Appl
39	17	1.1	20	3	US-08-873-437-3	Sequence 3, Appl
40	17	1.1	20	4	US-09-417-090-9	Sequence 9, Appl
41	17	1.1	20	4	US-09-727-578-9	Sequence 9, Appl
42	17	1.1	20	4	US-09-662-235-5	Sequence 5, Appl
43	17	1.1	22	1	US-08-033-837A-3	Sequence 3, Appl
44	17	1.1	22	1	US-08-374-983A-3	Sequence 3, Appl
45	17	1.1	24	3	US-09-126-280-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-462-484-3
; Sequence 3, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Asalyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56675310 No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowrey, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/POCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron

; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1133..1187
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1284..1342
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1752..1815
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1873..1928
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2136..2195
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(364..543, 593..661, 716..835, 900..1013,
; 1067..1132, 1188..1283, 1343..1498, 1554..1751,
; 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1499..1553
; US-08-462-484-3

Query Match 16.4%; Score 246; DB 1; Length 2880;
Best Local Similarity 99.7%; Pred. No. 5.4e-106;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1204 CAGCCCTTCGCGTTCGTCAGCGGGGAGCACACGTATACTACACGACCCGATC 1263
Db 2196 CAGCCCTTCGCGTTCGTCAGCGGGGAGCACACGTATACTACACGACCCGATC 2255
QY 1264 TTCGGCAGCTCGTGACGACGGGACGCGCGCGGGGACACGTCAGATCCGCTTC 1323
Db 2256 TTCGGCAGCTCGTGACGACGGGACGCGCGCGGGGACACGTCAGATCCGCTTC 2315
QY 1324 CAGACGGACAAACCCCGCGTGTCTCCACTGCGACATCGACTTCCACCTCGACGCG 1383
Db 2316 CAGACGGACAAACCCCGCGTGTCTCCACTGCGACATCGACTTCCACCTCGACGCA 2375
QY 1384 GGCTTCGGATCGTTCGACAGGAGCGTTGCGGACGTGAGGCGGCGAACCCTTCG 1443
Db 2376 GGCTTCGGATCGTTCGACAGGAGCGTTGCGGACGTGAGGCGGCGAACCCTTCG 2435
QY 1444 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGACGAGGCTAACAGTGA 1500
Db 2436 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGACGAGGCTAACAGTGA 2492

RESULT 2

US-08-441-147-3
; Sequence 3; Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalborge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5770418 of No. 5770418 of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron
; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1133..1187
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1284..1342
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1752..1815
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1873..1928
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2136..2195
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(364..543, 593..661, 716..835, 900..1013,
; 1067..1132, 1188..1283, 1343..1498, 1554..1751,
; 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1499..1553
; US-08-441-147-3

Query Match 16.4%; Score 246; DB 1; Length 2880;
Best Local Similarity 99.7%; Pred. No. 5.4e-106;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1204 CAGCCCTTCGCGTTCGTCAGCGGGGAGCACACGTATACTACACGACCCGATC 1263
Db 2196 CAGCCCTTCGCGTTCGTCAGCGGGGAGCACACGTATACTACACGACCCGATC 2255
QY 1264 TTCGGCAGCTCGTGACGACGGGACGCGCGGGGACACGTCAGATCCGCTTC 1323
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;; FILING DATE: 15-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.010-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9655
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Polyporus pinsitus
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 414..464
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 534..589
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 710..764
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 879..934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1001..1050
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1147..1197
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1354..1410
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1609..1662
;; NAME/KEY: CDS
;; LOCATION: join (413..465, 533..590, 709..765, 878..935,
;; LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
US-08-462-484-1

Query Match 2.5% Score 38; DB 1; Length 2418;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1379
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Db 2065 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 5

US-08-441-147-1
; Sequence 1, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Paule
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York

;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/441.147
;; FILING DATE: 15-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.010-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9655
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2418 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Polyporus pinsitus
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 414..464
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 534..589
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 710..764
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 879..934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1001..1050
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1147..1197
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1354..1410
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1609..1662
;; NAME/KEY: CDS
;; LOCATION: join (413..465, 533..590, 709..765, 878..935,
;; LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
US-08-441-147-1

Query Match 2.5% Score 38; DB 1; Length 2418;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 2065 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 6

PCT-US95-07536-1
; Sequence 1, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07536
FILING DATE: 15-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
FILING DATE: 24-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.204-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2418 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
NAME/KEY: intron
LOCATION: 414..464
FEATURE:
NAME/KEY: intron
LOCATION: 534..589
FEATURE:
NAME/KEY: intron
LOCATION: 710..764
FEATURE:
NAME/KEY: intron
LOCATION: 879..934
FEATURE:
NAME/KEY: intron
LOCATION: 1001..1050
FEATURE:
NAME/KEY: intron
LOCATION: 1147..1197
FEATURE:
NAME/KEY: intron
LOCATION: 1354..1410
FEATURE:
NAME/KEY: intron
LOCATION: 1609..1662
FEATURE:
NAME/KEY: CDS
LOCATION: join (413..465, 533..590, 709..765, 878..935,
1000..1051, 1146..1198, 1353..1411, 1608..1663)
PCT-US95-07536-1

Query Match 2.5% Score 38; DB 5; Length 2418;
Best Local Similarity 100.08; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
DB 2065 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 7
US-08-462-484-9
Sequence 9, Application US/08462484
Patent No. 5667531
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Xu, Feng
APPLICANT: Dalboge, Henrik
APPLICANT: Schneider, Falle
APPLICANT: Aslyng, Dorrit A.
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,484
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,147
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
NAME/KEY: intron
LOCATION: 734..808
FEATURE:
NAME/KEY: intron
LOCATION: 878..932
FEATURE:
NAME/KEY: intron
LOCATION: 1051..1104
FEATURE:
NAME/KEY: intron
LOCATION: 1219..1270
FEATURE:
NAME/KEY: intron
LOCATION: 1336..1397
FEATURE:
NAME/KEY: intron
LOCATION: 1713..1744
FEATURE:
NAME/KEY: intron
LOCATION: 2030..2085
FEATURE:
NAME/KEY: intron
LOCATION: 2308..2375

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; NAME/KEY: intron
; LOCATION: 2492..2569
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271,
; LOCATION: 2542..2600).
; US-08-462-484-9
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Query Match      2.3%  Score 35; DB 1; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2587 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 2621
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RESULT 8
US-08-441-147-9
; Sequence 9, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palie
; APPLICANT: Aaslynd, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
; FEATURE:
; NAME/KEY: intron
; LOCATION: 734..808
; FEATURE:
; NAME/KEY: intron
; LOCATION: 878..932
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1051..1104
; FEATURE:
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; NAME/KEY: intron
; LOCATION: 1219..1270
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; NAME/KEY: intron
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; FEATURE:
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; NAME/KEY: intron
; LOCATION: 2308..2375
; FEATURE:
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; NAME/KEY: intron
; LOCATION: 2492..2569
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271,
; LOCATION: 2542..2600).
; US-08-441-147-9
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Query Match      2.3%  Score 35; DB 1; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 2587 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 2621
```

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RESULT 9
PCT-US95-07536-9
; Sequence 9, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
```

FEATURE:
NAME/KEY: intron
LOCATION: 734..808
FEATURE:
NAME/KEY: intron
LOCATION: 878..932
FEATURE:
NAME/KEY: intron
LOCATION: 1051..1104
FEATURE:
NAME/KEY: intron
LOCATION: 1219..1270
FEATURE:
NAME/KEY: intron
LOCATION: 1336..1397
FEATURE:
NAME/KEY: intron
LOCATION: 1713..7744
FEATURE:
NAME/KEY: intron
LOCATION: 2030..2085
FEATURE:
NAME/KEY: intron
LOCATION: 2308..2375
FEATURE:
NAME/KEY: intron
LOCATION: 2492..2569
FEATURE:
NAME/KEY: CDS
LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271, 2542..2600).
PCT-US95-07536-9

Query Match 2.3%; Score 35; DB 5; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CGTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 2587 CGTGGTTCCTCCACTGCCACATCGACTTCCACCT 2621

RESULT 10

US-08-462-484-7

Sequence 7, Application US/08462484

Patent No. 5667531

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,484

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/441,147

FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: intron
LOCATION: 851..905
FEATURE:
NAME/KEY: intron
LOCATION: 1266..1320
FEATURE:
NAME/KEY: intron
LOCATION: 1351..1376
FEATURE:
NAME/KEY: intron
LOCATION: 1416..1468
FEATURE:
NAME/KEY: intron
LOCATION: 1625..1683
FEATURE:
NAME/KEY: intron
LOCATION: 1882..1934
FEATURE:
NAME/KEY: intron
LOCATION: 2202..2252
FEATURE:
NAME/KEY: intron
LOCATION: 2370..2425
FEATURE:
NAME/KEY: intron
LOCATION: 2543..2599
FEATURE:
NAME/KEY: CDS
LOCATION: join(540..725, 782..850, 906..1025, 1086..1265, 1321..1350, 1377..1415, 1469..1624, 1684..1881, 1935..2201, 2253..2369, 2426..2542, 2600..2653)
US-08-462-484-7

Query Match 2.0%; Score 30; DB 1; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1345 TGGTTCCTCCACTGCCACATCGACTTCCAC 1374
|||||

Db 2444 TGGTTCCTCCACTGCCACATCGACTTCCAC 2473

RESULT 11

US-08-441-147-7

Sequence 7, Application US/08441147

Patent No. 5770418

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/441,147
;; FILING DATE: 15-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.010-US
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9655
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2860 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 851..905
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1266..1320
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1351..1376
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1416..1468
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1625..1683
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1882..1934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2202..2252
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2370..2425
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2543..2599
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(540..725, 782..850, 906..1025, 1086..1265,
;; LOCATION: 1321..1350, 1377..1415, 1469..1624, 1684..1881,
;; LOCATION: 1935..2201, 2253..2369, 2426..2542, 2600..2653)
US-08-441-147-7

Query Match 2.0%; Score 30; DB 1; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1345 TGGTTCCTCCACTGCCACATCGACTTCCAC 1374

Db 2444 TGGTTCCTCCACTGCCACATCGACTTCCAC 2473

RESULT 12
PCT-US95-07536-7
; Sequence 7, Application PC/TUS9507536
; GENERAL INFORMATION:

;; APPLICANT:
;; APPLICANT:
;; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
;; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Novo Nordisk of North America, Inc.
;; STREET: 405 Lexington Avenue, Suite 6400
;; COUNTRY: U.S.A.
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/07536
;; FILING DATE: 15-June-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/265,534
;; FILING DATE: 24-June-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.204-WO
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9655
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2860 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 851..905
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1266..1320
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1351..1376
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1416..1468
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1625..1683
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1882..1934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2202..2252
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2370..2425
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2543..2599
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(540..725, 782..850, 906..1025, 1086..1265,
;; LOCATION: 1321..1350, 1377..1415, 1469..1624, 1684..1881,
;; LOCATION: 1935..2201, 2253..2369, 2426..2542, 2600..2653)
PCT-US95-07536-7

Query Match 2.0%; Score 30; DB 5; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1345 TGGTTCCTCCACTGCCACATCGACTTCCAC 1374

Db 2444 TGGTCTCCACTGCCACATCGACTTCCAC 2473
|||||

RESULT 13

US-08-462-484-5

Sequence 5, Application US/08462484

Patent No. 5667531

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,484

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/441,147

FILING DATE: 15-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4185.010-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 878 9655

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3102 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Polyporus pinsitus

FEATURE:

NAME/KEY: intron

LOCATION: 666..720

FEATURE:

NAME/KEY: intron

LOCATION: 790..845

FEATURE:

NAME/KEY: intron

LOCATION: 1125..1182

FEATURE:

NAME/KEY: intron

LOCATION: 1390..1450

FEATURE:

NAME/KEY: intron

LOCATION: 1607..1661

FEATURE:

NAME/KEY: intron

LOCATION: 1863..1918

FEATURE:

NAME/KEY: intron

LOCATION: 1976..2025

FEATURE:

NAME/KEY: intron

LOCATION: 2227..2285

FEATURE:

NAME/KEY: intron

LOCATION: 2403..2458

FEATURE:

NAME/KEY: intron

LOCATION: 2576..2627

FEATURE:

NAME/KEY: CDS

LOCATION: Join (665..721, 789..846, 1124..1183, 1389..1451,

LOCATION: 1606..1662, 1862..1919, 1975..2026, 2226..2286, 2402..2459,

LOCATION: 2575..2628).

US-08-462-484-5

Query Match

Best Local Similarity 1.6%; Score 24; DB 1; Length 3102;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 ATCAACTCGCCATCTCGGCTAC 843

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Db 1754 ATCAACTCGCCATCTCGGCTAC 1777

RESULT 14

US-08-441-147-5

Sequence 5, Application US/08441147

Patent No. 5770418

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,147

FILING DATE: 15-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4185.010-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 878 9655

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3102 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Polyporus pinsitus

FEATURE:

NAME/KEY: intron

LOCATION: 666..720

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FEATURE:
NAME/KEY: intron
LOCATION: 790..845
FEATURE:
NAME/KEY: intron
LOCATION: 1125..1182
FEATURE:
NAME/KEY: intron
LOCATION: 1390..1450
FEATURE:
NAME/KEY: intron
LOCATION: 1607..1661
FEATURE:
NAME/KEY: intron
LOCATION: 1863..1918
FEATURE:
NAME/KEY: intron
LOCATION: 1976..2025
FEATURE:
NAME/KEY: intron
LOCATION: 2227..2285
FEATURE:
NAME/KEY: intron
LOCATION: 2403..2458
FEATURE:
NAME/KEY: intron
LOCATION: 2576..2627
FEATURE:
NAME/KEY: CDS
LOCATION: join (665..721, 789..846, 1124..1183, 1389..1451,
LOCATION: 1606..1662, 1862..1919, 1975..2026, 2226..2286, 2402..2459,
LOCATION: 2575..2628).
US-08-441-147-5
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Query Match 1.6%; Score 24; DB 1; Length 3102;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 820 ATCAACTCCGCCATCTCGCGCTAC 843
|||||
Db 1754 ATCAACTCCGCCATCTCGCGCTAC 1777
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RESULT 15

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PCT-US95-07536-5
Sequence 5, Application PC/TUS9507536
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07536
FILING DATE: 15-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
FILING DATE: 24-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185,204-WO
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 666..720
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 790..845
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 1125..1182
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 1390..1450
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 1607..1661
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 1863..1918
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 1976..2025
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 2227..2285
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 2403..2458
FEATURE:
```

```
NAME/KEY: intron
LOCATION: 2576..2627
FEATURE:
```

```
NAME/KEY: CDS
LOCATION: join (665..721, 789..846, 1124..1183, 1389..1451,
LOCATION: 1606..1662, 1862..1919, 1975..2026, 2226..2286, 2402..2459,
LOCATION: 2575..2628).
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PCT-US95-07536-5
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Query Match 1.6%; Score 24; DB 5; Length 3102;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 820 ATCAACTCCGCCATCTCGCGCTAC 843
|||||
Db 1754 ATCAACTCCGCCATCTCGCGCTAC 1777
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Search completed: December 14, 2002, 06:56:05
Job time : 117 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:53:32 ; Search time 65 Seconds
(without alignments)
9126.023 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgccggtggcgag.....tgagcgaggtaaccagtga 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 355320 seqs, 197730502 residues

Word size : 0

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	1.4	590	10	US-09-917-800A-1579
c 2	20	1.3	533	9	Sequence 1579, Ap
c 3	20	1.3	768	9	Sequence 66, Appl
c 4	19	1.3	1383	10	Sequence 58, Appl
c 5	19	1.3	1749	10	Sequence 9610, Ap
c 6	19	1.3	1864	9	Sequence 149, App
c 7	19	1.3	1892	12	Sequence 43, Appl
c 8	19	1.3	3405	9	Sequence 793, App
c 9	19	1.3	3405	9	Sequence 44, Appl
c 10	18	1.2	227	10	Sequence 36, Appl
c 11	18	1.2	273	10	Sequence 4004, Ap
c 12	18	1.2	1503	9	Sequence 3898, Ap
c 13	18	1.2	397658	10	Sequence 128, App
c 14	17	1.1	17	10	Sequence 3, Appli
c 15	17	1.1	18	10	Sequence 2, Appli
c 16	17	1.1	19	9	Sequence 15, Appl
c 17	17	1.1	22	10	Sequence 4, Appli
c 18	17	1.1	24	10	Sequence 20, Appl
c 19	17	1.1	33	9	Sequence 19, Appl
					Sequence 10, Appl

c 20	17	1.1	52	10	US-09-775-217-7	Sequence 7, Appli
c 21	17	1.1	54	10	US-09-783-590-3459	Sequence 3459, Ap
c 22	17	1.1	57	10	US-09-955-849-4	Sequence 4, Appli
c 23	17	1.1	57	10	US-09-973-013-4	Sequence 1, Appli
c 24	17	1.1	62	10	US-09-557-423-1	Sequence 5, Appli
c 25	17	1.1	76	10	US-09-557-423-5	Sequence 3, Appli
c 26	17	1.1	81	10	US-09-557-423-3	Sequence 3335, Ap
c 27	17	1.1	88	10	US-09-783-590-3235	Sequence 3334, Ap
c 28	17	1.1	100	10	US-09-783-590-3234	Sequence 737, App
c 29	17	1.1	105	10	US-09-924-035A-737	Sequence 717, Ap
c 30	17	1.1	105	10	US-09-974-300-7717	Sequence 9, Appli
c 31	17	1.1	118	10	US-09-784-130-9	Sequence 713, App
c 32	17	1.1	132	10	US-09-924-035A-713	Sequence 659, App
c 33	17	1.1	133	10	US-09-924-035A-659	Sequence 675, App
c 34	17	1.1	143	10	US-09-924-035A-675	Sequence 6, Appli
c 35	17	1.1	145	10	US-09-822-250-6	Sequence 2, Appli
c 36	17	1.1	145	10	US-09-987-456-2	Sequence 808, App
c 37	17	1.1	145	10	US-09-924-035A-808	Sequence 7, Appli
c 38	17	1.1	148	10	US-09-822-250-7	Sequence 3, Appli
c 39	17	1.1	148	10	US-09-987-456-3	Sequence 8, Appli
c 40	17	1.1	149	10	US-09-822-250-8	Sequence 4, Appli
c 41	17	1.1	149	10	US-09-987-456-4	Sequence 9, Appli
c 42	17	1.1	150	10	US-09-822-250-9	Sequence 5, Appli
c 43	17	1.1	180	10	US-09-987-456-5	Sequence 24463, A
c 44	17	1.1	202	10	US-09-864-761-24463	Sequence 693, App
c 45	17	1.1			US-09-924-035A-693	

ALIGNMENTS

RESULT 1
US-09-917-800A-1579
; Sequence 1579, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917.800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1579
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012838
US-09-917-800A-1579

Query Match 1.4%; Score 21; DB 10; Length 590;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 999 CGGACCAACTTCTTCATCAA 1019
|||||
Db 236 CGGACCAACTTCTTCATCAA 256

RESULT 2

US-09-996-140-66/c
; Sequence 66, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
; APPLICANT: Thomasow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Ottosen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-Zhong
; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL

STRESS TOLERANCE

; FILE REFERENCE: MBI0040US

; CURRENT APPLICATION NUMBER: US/09/996,140

; CURRENT FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 09/706,270

; PRIOR FILING DATE: 1996-09-04

; PRIOR APPLICATION NUMBER: 09/018,233

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/017,816

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,235

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/017,575

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,227

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,234

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/198,119

; PRIOR FILING DATE: 1998-11-23

; PRIOR APPLICATION NUMBER: PCT/US99/01895

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 66

; LENGTH: 533

; TYPE: DNA

; ORGANISM: Brassica oleracea

US-09-996-140-66

Query Match 1.3%; Score 20; DB 9; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1268 GCGACGTCGTGAGCAGCGGC 1287
|||||
Db 353 GCGACGTCGTGAGCAGCGGC 334

RESULT 3

US-09-996-140-58/c

; Sequence 58, Application US/09996140

; Patent No. US20020157136A1

; GENERAL INFORMATION:

; APPLICANT: Thomasow, Michael

; APPLICANT: Stockinger, Eric

; APPLICANT: Jaglo-Ottosen, Kirsten

; APPLICANT: Gilmour, Sarah

; APPLICANT: Zarka, Daniel

; APPLICANT: Jiang, Cai-Zhong

; TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL

; TITLE OF INVENTION: STRESS TOLERANCE

; FILE REFERENCE: MBI0040US

; CURRENT APPLICATION NUMBER: US/09/996,140

; CURRENT FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 09/706,270

; PRIOR FILING DATE: 1996-09-04

; PRIOR APPLICATION NUMBER: 09/018,233

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/017,816

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,235

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/017,575

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,227

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/018,234

; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: 09/198,119

; PRIOR FILING DATE: 1998-11-23

; PRIOR APPLICATION NUMBER: PCT/US99/01895

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 58

; LENGTH: 768

; TYPE: DNA

; ORGANISM: Brassica napus

US-09-996-140-58

Query Match 1.3%; Score 20; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1268 GCGACGTCGTGAGCAGCGGC 1287
|||||
Db 302 GCGACGTCGTGAGCAGCGGC 283

RESULT 4

US-09-815-242-9610/c

; Sequence 9610, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9610
LENGTH: 1383
TYPE: DNA
ORGANISM: Salmonella typhi
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1383)
NAME/KEY: misc_feature
LOCATION: (1)...(1383)
OTHER INFORMATION: n = A,T,C or G
US-09-815-242-9610

Query Match 1.3%; Score 19; DB 10; Length 1383;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 GACTTTCACGCCGCCGACC 1044
|||||
DB 1104 GACTTTCACGCCGCCGACC 1086

RESULT 5

US-09-923-779-149/c
Sequence 149, Application US/09923779
Patent No. US20020076721A1

GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 149
LENGTH: 1749
TYPE: DNA
ORGANISM: Homo sapiens
US-09-923-779-149

Query Match 1.3%; Score 19; DB 10; Length 1749;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||
DB 812 TCCACCTCGACGGCGCTT 794

RESULT 6

US-09-974-298-43/c
Sequence 43, Application US/09974298
Patent No. US20020156263A1

GENERAL INFORMATION:
APPLICANT: Chen, Hwei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program

SEQ ID NO 43
LENGTH: 1864
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 127987.19
US-09-974-298-43

Query Match 1.3%; Score 19; DB 9; Length 1864;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||
DB 660 TCCACCTCGACGGCGCTT 642

RESULT 7

US-10-044-090-793/c
Sequence 793, Application US/10044090
Patent No. US20020137081A1

GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 793
LENGTH: 1892
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 2812002CB1
US-10-044-090-793

Query Match 1.3%; Score 19; DB 12; Length 1892;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||
DB 675 TCCACCTCGACGGCGCTT 657

RESULT 8

US-09-974-298-44/c
Sequence 44, Application US/09974298
Patent No. US20020156263A1

GENERAL INFORMATION:
APPLICANT: Chen, Hwei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 44
LENGTH: 3405
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1397781.7
US-09-974-298-44

Query Match 1.3%; Score 19; DB 9; Length 3405;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||
DB 802 TCCACCTCGACGGCGCTT 784

RESULT 9

US-09-981-353-36/C
; Sequence 36, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1397781.7
US-09-981-353-36

Query Match 1.3%; Score 19; DB 9; Length 3405;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGCGGCTT 1388
|||||
DB 802 TCCACCTCGACGCGGCTT 784

RESULT 10
US-09-294-093B-4004
; Sequence 4004, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4004
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700352953H1
US-09-294-093B-4004

Query Match 1.2%; Score 18; DB 10; Length 227;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 CAAGCGCACGAGTCGCC 861
|||||
DB 185 CAAGCGCACGAGTCGCC 202

RESULT 11
US-09-294-093B-3898
; Sequence 3898, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3898
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700352769H1
US-09-294-093B-3898

Query Match 1.2%; Score 18; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 CAAGCGCACGAGTCGCC 861
|||||
DB 185 CAAGCGCACGAGTCGCC 202

RESULT 12
US-09-712-363-128
; Sequence 128, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Edward M.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-128

Query Match 1.2%; Score 18; DB 9; Length 1503;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1146 CACGCTGCCGCGACCGC 1163
|||||
DB 820 CACGCTGCCGCGACCGC 837

RESULT 13

US-09-813-320-3/c
; Sequence 3, Application US/09813320
; Patent No. US20020142378A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Hongyu et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001172
; CURRENT APPLICATION NUMBER: US/09/813,320
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 397658
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(397658)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-320-3

Query Match 1.2%; Score 18; DB 10; Length 397658;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CACGGCTTCTCCAGGCA 213

Db 100446 CACGGCTTCTCCAGGCA 100429

RESULT 14

US-09-946-376-2
; Sequence 2, Application US/09946376
; Patent No. US20020115146A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Jae-Gu
; APPLICANT: Jung, Hueng-Chae
; TITLE OF INVENTION: Method of Protein Synthesis
; FILE REFERENCE: 10981-003-999
; CURRENT APPLICATION NUMBER: US/09/946,376
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 00-52464
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-946-376-2

Query Match 1.1%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

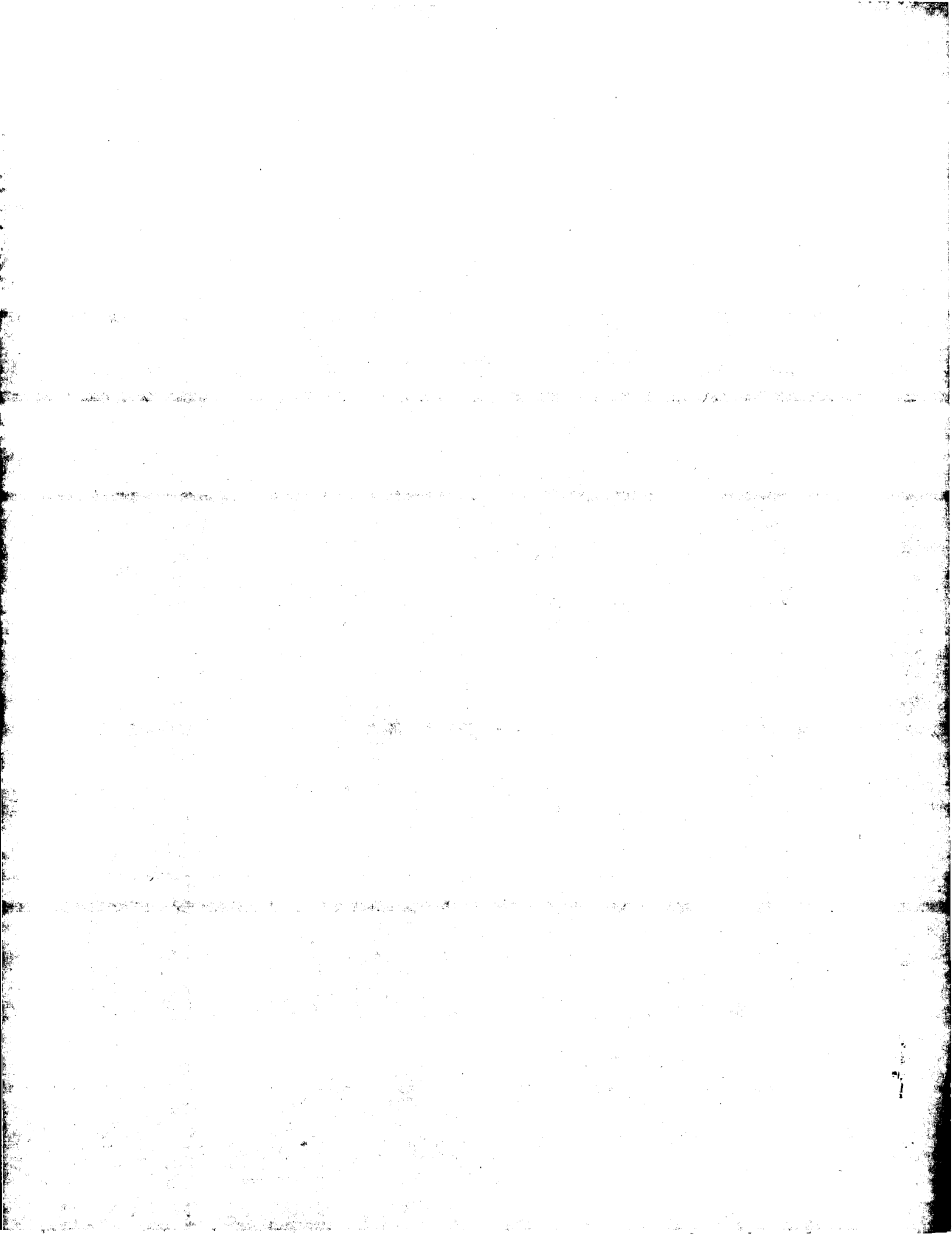
QY 662 TCGAGGTCGACGGTATC 678

Db 1 TCGAGGTCGACGGTATC 17

RESULT 15

US-09-855-999-15
; Sequence 15, Application US/09855999
; Patent No. US20020119456A1
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; Tabone, John C.
; Howbert, J. Jeffrey

Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETERMINING
; THE SEQUENCE OF NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED INTELLECTUAL PROPERTY LAW GROUP PLLC
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/855,999
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David W.
; REGISTRATION NUMBER: 37,414
; REFERENCE/DOCKET NUMBER: 780068.416C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-855-999-15
Query Match 1.1%; Score 17; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 662 TCGAGGTCGACGGTATC 678
Db 1 TCGAGGTCGACGGTATC 17
Search completed: December 14, 2002, 08:34:43
Job time : 720 secs



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OM protein - protein search, using sw model

Run on: December 14, 2002, 06:56:12 ; Search time 26 Seconds
(without alignments)
796.026 Million cell updates/sec

Title: US-09-786-960-2

Perfect score: 2669

Sequence: 1 AIGPVASLVANAPVSPDGF.....VPKAWSDLCPIYDGLSEANQ 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2656	99.5	519	1	LAC2_TRAVI
3	2243	84.0	520	1	LAC1_CORHI
4	2194	82.2	520	1	LAC1_TRAVI
5	1917.5	71.8	527	1	LAC5_TRAVI
6	1916.5	71.8	527	1	LAC5_TRAVE
7	1882.5	70.5	520	1	LAC4_TRAVE
8	1871.5	70.1	520	1	LAC4_TRAVI
9	1743.5	65.3	529	1	LAC1_PLEOS
10	1743.5	65.3	533	1	LAC2_PLEOS
11	1716	64.3	548	1	LAC1_PHLRA
12	1606.5	60.2	473	1	LAC3_TRAVI
13	1219.5	45.7	520	1	LAC2_AGABI
14	1192.5	44.7	520	1	LAC1_AGABI
15	1077	40.4	531	1	LAC4_THACU
16	992	37.2	599	1	LAC2_THACU
17	930.5	34.9	572	1	LAC3_THACU
18	901	33.8	576	1	LAC1_THACU
19	622.5	23.3	621	1	LAC2_PODAN
20	614.5	23.0	624	1	LAC3_CANAL
21	607.5	22.8	591	1	LAC1_CRYPA
22	601.5	22.5	619	1	LAC1_NEUCR
23	600.5	22.5	619	1	LAC2_NEUCR
24	599	22.4	636	1	FET3_YEAST
25	597.5	22.4	622	1	FET5_YEAST
26	583.5	21.9	486	1	LAC1_BOTCI
27	556	20.8	622	1	YAK8_SCHPO
28	536.5	20.1	587	1	ASO_CUCSA
29	530.5	19.9	578	1	ASO_TOBAC
30	510	19.1	552	1	ASO_CUCPM
31	501	18.8	579	1	ASO_CUCMA
32	392	14.7	608	1	YD56_YEAST
33	333	12.5	609	1	LAC1_EMENI

ALIGNMENTS

RESULT 1

LAC2_TRAVE

ID LAC2_TRAVE STANDARD; PRT; 519 AA.

AC Q12718: Q12716;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)

DE (Urishiol oxidase) (Diphenol oxidase) (Laccase I).

GN LCC2 OR LCCI

OS Trametes versicolor (White-rot fungus).

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Aphyllophorales; Trametes.

OX NCBI_TaxID=5325;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=52J;

RX MEDLINE=97464057; PubMed=9322748;

RA Ong E., Pollock W.B., Smith M.;

RT "Cloning and sequence analysis of two laccase complementary DNAs from the ligninolytic basidiomycete Trametes versicolor.";

RL Gene 196:113-119(1997).

CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED

CC PRODUCTS (PROBABLE).

CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2

CC H(2)O.

CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU

CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE

CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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CC EMBL: U44851; AAA86659.1; -

CC EMBL: U44430; AAC49828.1; -

CC HSP; F37064; IAOZ.

CC InterPro: IPR001117; Cu-oxidase.

CC InterPro: IPR002355; MultiCu_oxidase2.

CC Pfam: PF00394; Cu-oxidase; 3.

CC PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.

CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.

CC Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

CC Lignin degradation; Multigene family.

CC SIGNAL 1 20 POTENTIAL.

CC CHAIN 21 519 LACCASE 2.

CC DOMAIN 22 147 PLASTOCYANIN-LIKE 1.

CC DOMAIN 159 301 PLASTOCYANIN-LIKE 2.

CC DOMAIN 368 490 PLASTOCYANIN-LIKE 3.

34 272 10.2 555 1 ASO_BRANA
35 271.5 10.2 605 1 PCOA_ECOLI
36 270.5 10.1 609 1 COPA_PESM
37 266 10.0 554 1 NTP3_TOBAC
38 207 7.8 572 1 BLRO_MYRVE
39 173.5 6.5 513 1 COTA_WACSU
40 166.5 6.2 516 1 CUEO_ECOLI
41 164.5 6.2 516 1 CUEO_ECO57
42 155.5 5.8 533 1 CUEO_YERPE
43 138.5 5.2 536 1 CUEO_SALTI
44 138.5 5.2 536 1 CUEO_SALTY
45 126 4.7 470 1 SUFI_ECOLI

Q00624 brassica na
Q47452 escherichia
P12374 pseudomonas
P29162 nicotiana t
Q12737 myrothecium
P07788 bacillus su
P36649 escherichia
Q8X947 escherichia
Q8ZBK0 yersinia pe
Q8Z9E1 salmonella
Q8ZRS2 salmonella
P26648 escherichia

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FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 69 69 D -> V (IN REF. 1: AAC49828).
SQ SEQUENCE 519 AA; 55810 MW; BFFB5B4CD0007702 CRC64;

Query Match 99.7%; Score 2662; DB 1; Length 519;
Best Local Similarity 99.8%; Pred. No. 8.2e-183;
Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAVSPDGFRLDAIVNGVVPSPPLITCKGDRQLNVVDLTNHSMLKS 60
Db 21 AIGPVASLVANAVSPDGFRLDAIVNGVVPSPPLITCKGDRQLNVVDLTNHSMLKS 80
Qy 61 TSIHWGHFFOAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGL 120
Db 81 TSIHWGHFFOAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGL 140
Qy 121 RGPFFVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPFPPLGADATLNGLSRST 180
Db 141 RGPFFVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPFPPLGADATLNGLSRST 200
Qy 181 PTAALAVINVOHGKRYRRLYSISCDPNYTESIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 201 PTAALAVINVOHGKRYRRLYSISCDPNYTESIDGHNLTVEVDGINSQPLLVDSIQIFA 260
Qy 241 AQRYSFVLNANOTGVNWRANPNFTGVGFAGGINSALTRYOGAPVABPTTTQTTSTVPL 300
Db 261 AQRYSFVLNANOTGVNWRANPNFTGVGFAGGINSALTRYOGAPVABPTTTQTTSTVPL 320
Qy 301 IETNLHPLARMPVPGSPPTGGVDKALNLAENFNGTNEFINNATFTPTVPVLLQILSGAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAENFNGTNEFINNATFTPTVPVLLQILSGAQ 380
Qy 361 TAQDLLPAGSVYPLPAHSTIETLPATAPAGPHFPHLGHFAFVRSAGSTTYNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPATAPAGPHFPHLGHFAFVRSAGSTTYNYNDP 440
Qy 421 IFRDVSVTGTGAAGDNVTIRFQTDNPGPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVSVTGTGAAGDNVTIRFQTDNPGPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 2
LAC2_TRAVI
ID LAC2_TRAVI STANDARD; PRT; 519 AA.
AC Q99046;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
```

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GN LCC2.
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OX Aphyllophorales; Trametes.
RN NCBI_TaxID=47662;
RP [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Mycelium;
RC MEDLINE=97076915; PubMed=8975613;
RA Yaver D.S., Xu F., Gollightly E.J., Brown K.M., Brown S.H.,
RA Rey M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.;
RT "Purification, characterization, molecular cloning, and expression of
RT two laccase genes from the white rot basidiomycete Trametes
RT villosa.";
RL Appl. Environ. Microbiol. 62:834-841(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L49377; AAC41687.1; -.
DR HSP; P37064; LAC2.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 519 LACCASE 2.
FT DOMAIN 22 147 PLASTOCYANIN-LIKE 1.
FT DOMAIN 159 301 PLASTOCYANIN-LIKE 2.
FT DOMAIN 368 490 PLASTOCYANIN-LIKE 3.
FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 519 AA; 55777 MW; DBB4EA526F684740 CRC64;

Query Match 99.5%; Score 2656; DB 1; Length 519;
Best Local Similarity 99.4%; Pred. No. 2.2e-182;
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Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPSPDGLRDAIVVNGVVPSPDLITGKGGDRFQNLNVVDITLNNHSLKLS 60
Db 21 AIGPVASLVVANAPSPDGLRDAIVVNGVVPSPDLITGKGGDRFQNLNVVDITLNNHSLKLS 80
QY 61 TSHHGHFFQAGTNWADGPAFVNOCPISAGSHSLYDFHVPDQAGTFWYHSHLSSTQYCDGL 120
Db 81 TSHHGHFFQAGTNWADGPAFVNOCPISAGSHSLYDFHVPDQAGTFWYHSHLSSTQYCDGL 140
QY 121 RGFVVYDPRKPHASRYDNDNESTVITLTDWYHTAARLGPFRPLGADATLNLGLRSAST 180
Db 141 RGFVVYDPRKPHASRYDNDNESTVITLTDWYHTAARLGPFRPLGADATLNLGLRSAST 200
QY 181 PTAALAVINVQHGKRYRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 260
QY 241 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTQTTSVIPL 300
Db 261 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTQTTSVIPL 320
QY 301 IETNLHPLARMPVPGSPTGGVDKALNLFNFGTFFENNAFTPTPTVPLQLIILSGAQ 360
Db 321 IETNLHPLARMPVPGSPTGGVDKALNLFNFGTFFENNAFTPTPTVPLQLIILSGAQ 380
QY 361 TAQDLPLAGSVYPLPAHSTIETLPTALAPAGPFPFLHGHAFVAVRSAGSTTYNYNDP 420
Db 381 TAQDLPLAGSVYPLPAHSTIETLPTALAPAGPFPFLHGHAFVAVRSAGSTTYNYNDP 440
QY 421 IFRDVTSTGTPAAGDNVTRFQDNPFPWFLHGHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVTSTGTPAAGDNVTRFQDNPFPWFLHGHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PRAWSDLCPYDGLSEANQ 499
Db 501 PRAWSDLCPYDGLSEANQ 519

RESULT 3
LAC1CORHI
ID LAC1CORHI STANDARD; PRT; 520 AA.
AC Q02497;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Ligninolytic phenoloxidase).
OS Coriolus hirsutus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriolus.
ON NCBI_TaxID=5327;
RX STRAIN=IFO 4917;
RX MEDLINE=90368706; PubMed=2394718;
RA Kojima Y., Tsukuda Y., Kawai Y., Tsukamoto A., Sugura J.,
RA Sakano M., Kita Y.
RT "Cloning, sequence analysis, and expression of ligninolytic
RT phenoloxidase genes of the white-rot basidiomycete Coriolus
RT hirsutus."
RL J. Biol. Chem. 265:15224-15230(1990).
CC -!- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN
CC DEGRADATION. CLEAVES THE C-C AND C-O BONDS OF SOME PHENOLIC LIGNIN
CC MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS, AMINOPHENOLS AND
CC PHENYLENEDIAMINE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- POLYMORPHISM: 2 ALLELIC FORMS VARYING IN ONE AA POSITION.
```

```
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M60560: AAA33103.1; -
CC EMBL; M60561: AAA33104.1; -
CC PIR; A35883; A35883.
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; MultiCu_oxidase2.
CC Pfam; PF00394; Cu-oxidase; 3.
CC PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
CC PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
CC Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
CC Glycoprotein; Repeat.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 520 LACCASE.
CC DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
CC DOMAIN 160 302 PLASTOCYANIN-LIKE 2.
CC DOMAIN 369 491 PLASTOCYANIN-LIKE 3.
CC METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 416 416 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
CC CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 229 229 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
CC DISULFID 106 509 POTENTIAL.
CC DISULFID 138 226 POTENTIAL.
CC VARIANT 411 411 A -> P.
CC CONFLICT 378 379 SG -> RR (IN REF. 1; AAA33104).
CC SEQUENCE 520 AA; 55688 MW; 977D8DFA551F7929 CRC64;
Query Match 84.0%; Score 2243; DB 1; Length 520;
Best Local Similarity 81.8%; Pred. No. 6.7e-153;
Matches 408; Conservative 35; Mismatches 56; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPSPDGLRDAIVVNGVVPSPDLITGKGGDRFQNLNVVDITLNNHSLKLS 60
Db 22 AIGPTADLATISNAEVSPPDGFARQAVVNVNTPGLVAGNKGDRFQNLNVNLTNNHSLKLS 81
QY 61 TSHHGHFFQAGTNWADGPAFVNOCPISAGSHSLYDFHVPDQAGTFWYHSHLSSTQYCDGL 120
Db 82 TSHHGHFFQAGTNWADGPAFVNOCPISAGSHSLYDFHVPDQAGTFWYHSHLSSTQYCDGL 141
QY 121 RGFVVYDPRKPHASRYDNDNESTVITLTDWYHTAARLGPFRPLGADATLNLGLRSAST 180
Db 142 RGFVVYDPRKPHASRYDNDNESTVITLTDWYHTAARLGPFRPLGADATLNLGLRSAST 201
QY 181 PTAALAVINVQHGKRYRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
Db 202 TAADLAVINVTKGKRYRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 261
QY 241 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTQTTSVIPL 300
```

Db 262 AQRYSVLNAQDVGNVIRANPNFNGVYFAGGINSAILRYDGDVPEPTTTQTTPKPL 321
QY 301 IETNLHPLARMPVPGSPGGVDKALNLAFAFNFTNNATETPTVPVVLQILSGAQ 360
Db 322 NEVDLHPLATMAVPGSPVAGGVDTAINAFNFTNFINGASFVPTVPVVLQILSGAQ 381
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPAGSVYSLPSNADIEISFPATAAPGAPHPFHLGHAFVAVRSAGSTTYNDP 441
QY 421 IFRDVVSTGTPAAGDNVTIRFOTDNPFGWFLHCHDFHLDAGFAIVFAEDVADYKAANPV 480
Db 442 IFRDVVSTGTPAAGDNVTIRFOTDNPFGWFLHCHDFHLDAGFAIVFAEDIPDVASANPV 501
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 502 QAWSDLCPYDALDVNDQ 520

RESULT 4
LACL_TRAVI
ID LACL_TRAVI STANDARD; PRT; 520 AA.
AC Q99044;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Laccase 1 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCCL

OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=47662;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mycelium;
RX MEDLINE=97076915; PubMed=9975613;
RA Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H.,
RA Rey M.W., Schneider P., Halkier T., Mondorf K., Balboge H.;
RT "Purification, characterization, molecular cloning, and expression of
RT two laccase genes from the white rot basidiomycete Trametes
RT villosa".
RL Appl. Environ. Microbiol. 62:834-841(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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EMBL; L49376; AAC41686.1; -;
DR HSSP; P37064; LAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
DR Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 520
FT DOMAIN 23 148
FT DOMAIN 160 302
FT DOMAIN 369 491
FT METAL 85 85
FT METAL 87 87
FT METAL 130 130
FT METAL 132 132
FT METAL 416 416
FT METAL 419 419
FT METAL 421 421
FT METAL 473 473
FT METAL 474 474
FT METAL 475 475
FT METAL 479 479
FT METAL ?
FT CARBOHYD 72 72
FT CARBOHYD 75 75
FT CARBOHYD 229 229
FT CARBOHYD 238 238
FT CARBOHYD 354 354
FT CARBOHYD 361 361
FT CARBOHYD 457 457
SQ SEQUENCE 520 AA; 55545 MW; 046AB6D74737C60E CRC64;

Query Match 82.2%; Score 2194; DB 1; Length 520;
Best Local Similarity 79.7%; Pred. No. 2.1e-149;
Matches 397; Conservative 36; Mismatches 65; Indels 0; Gaps 0;

QY 2 IGVASVLVANAAPVSPDGLFDRDAIVVGVSPPLITGKGGDRFQNLNVVDTLTNHSMLKST 61
Db 23 IGPVADLITITNAAVSPDGFSGRQAVVVGTPGLITGKGGDRFQNLNVDTLTNHSMLKST 82
QY 62 SIHWHGFFQAGTNWADGPAFVYNOCPFIASGHSFLYDFHVPDQAGTFWYHSHLSTQVCDGLR 121
Db 83 SIHWHGFFQAGTNWADGPAFVYNOCPFIASGHSFLYDFHVPDQAGTFWYHSHLSTQVCDGLR 142
QY 122 GPFVYVDPKPHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSASTP 181
Db 143 GPFVYVDPNDPAADLYDVNDNDTVITLVDWYHVAALGPAFPLGADATLNLGLRSASTP 202
QY 182 TAALAVINQHGKRYRFRFLVSIISCDPNYTFSDIGNLTVIEVDGINSOPLLVDSIQIFAA 241
Db 203 TADLSVSTPGKRYRFRFLVSLSCDPNYTFSDIGNLTVIEVDGINSOPLLVDSIQIFAA 262
QY 242 QRYSFVLNANQTVGNVVRANPNFCTGVFAGGINSAILRYOGAPVAEPTTTQTSVIFLI 301
Db 263 QRYSFVLEANAQVDNYWIRANPNFNGVGTGINSAILRYOGAAVEPTTTQTSVIFLI 322
QY 302 ETNLHPLARMPVPGSPPTGGVDKALNLAFAFNFTNNATETPTVPVVLQILSGAQ 361
Db 323 EVNLHPLVTTAVPGSPVAGGVDTAINAFNFTNFINGASFVPTVPVVLQILSGAQ 382
QY 362 AQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNDP 421
Db 383 AQDLLPAGSVYSLPSNADIEISFPATAAPGAPHPFHLGHAFVAVRSAGSTTYNDP 442
QY 422 IFRDVVSTGTPAAGDNVTIRFOTDNPFGWFLHCHDFHLDAGFAIVFAEDVADYKAANPV 481
Db 443 IFRDVVSTGTPAAGDNVTIRFOTDNPFGWFLHCHDFHLDAGFAIVFAEDIPDVASANPV 502
QY 482 KAWSDLCPYDGLSEANQ 499
Db 503 QAWSDLCPYDALDVNDQ 520

RESULT 5
LACL_TRAVI
ID LACL_TRAVI STANDARD; PRT; 527 AA.
AC Q99056;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Lignin degradation; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 520 LACCASE 4.
FT DOMAIN 24 149 PLASTOCYANIN-LIKE 1.
FT DOMAIN 161 303 PLASTOCYANIN-LIKE 2.
FT DOMAIN 370 491 PLASTOCYANIN-LIKE 3.
FT DISULFID 107 509 PROBABLE.
FT DISULFID 139 227 PROBABLE.
FT METAL 86 86 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 88 88 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 133 133 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 421 421 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 423 423 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 497 497 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 520 AA; 55643 MW; FC1032400E9DDFA4 CRC64;

Query Match 70.5%; Score 1882.5; DB 1; Length 520;
Best Local Similarity 69.1%; Pred. No. 3.6e-127;
Matches 345; Conservative 56; Mismatches 95; Indels 3; Gaps 2;

QY 1 AIGPVASLVVAVSPDGLRDAIVVGVPSPLITGKGRDQFQNLNVVDITLNHSMKLS 60
DB 23 AIGPVTDLISNADVSPDGFTRAALVANGVFCPLITGKGNQFNQINDLSNETMKS 82
QY 61 TSHHGHFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 83 TSHHGHFQKGNWADGAAFAVNCQPIATGNSFLYDFATDQAGTFWYHSHLSTQYCDGL 142
QY 121 RGPVYVDKPDHASYDYDNESTVITLTDVHTAARLGRPRPLGADATLNGLSRSAST 180
DB 143 RGPVYVDSPDHPADLYDVDDETIITLSDVHTAASLGAAFPFGSDSLINGLGRFAGG 202
QY 181 PTAALAVINVQHGKRYRFLVLSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 203 DSTDLAVITVEQGRYMRLLSLSCDPNVYFSDGHNMVTIEADAVNHEPLTVDSIQIVA 262
QY 241 AQRYSEVLNANTGVNWRANPNFCTGVGFAGGINSAILRYQCAPVAEPTTQTTSVIPL 300
DB 263 GQRYSEVLADQDIDNIFYRALPSAGTTFSDGGINSAIRLYSGASEVDTTETTSVLPL 322
QY 301 IETNLHPLARMVPVPGSPTPGVDKALNAFNNGTFFNNATFTPTTPVPLQLQLSGAQ 360
DB 323 DEANLVPLDSPAPGDPNIGVDYALNLDNFEDGTFFINDVSFVPTVPVLLQLSGTT 382
QY 361 TAODLLPAGSVPLPAHSTETITLPATAL-APGAPHPFLHGHAFVAVRSAGSTTYNYND 419
DB 383 SAADLLPSGLFALPSNSTIEISFPITATNAPGAPHPFLHGHGTFIVRTAGSTDNEVN 442
QY 420 PIFRDVWVGTGTAAGDNVIRFQTDNPGPWFHLCHIDFHDAGFAIVFAEDVADVKAAP 479
DB 443 PVHRDVVNTGT--AGDNVIRFQTDNPGPWFHLCHIDFHDAGFAIVFAEDVADVNTTT 500
QY 480 VPKAWSDLCPYDGLSEAN 498
DB 501 PSTAWEDLCPTYNALDSSD 519
RESULT 8
LAC4_TRAVI

ID LAC4_TRAVI STANDARD; PRT; 520 AA.
AC Q99055;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
GN (Urishiol oxidase) (Diphenol oxidase).
OS LCC4.
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=47662;
RN [1]
RX MEDLINE=97128774; PubMed=8973314;
RA Yaver D.S., Golightly E.J.;
RT "Cloning and characterization of three laccase genes from the
white-rot basidiomycete Trametes villosa: genomic organization of the
laccase gene family.";
RT Gene 181:95-102(1996).
RL -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L78077; AAB47734.1; -.
DR HSP; P37064; IASO.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; MultiCu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 520 LACCASE 4.
FT DOMAIN 24 149 PLASTOCYANIN-LIKE 1.
FT DOMAIN 161 303 PLASTOCYANIN-LIKE 2.
FT DOMAIN 370 491 PLASTOCYANIN-LIKE 3.
FT METAL 86 86 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 88 88 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 133 133 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 421 421 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 423 423 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 497 497 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 520 AA; 55643 MW; 16469DC547C61F3C CRC64;

```
Query Match 70.1%; Score 1871.5; DB 1; Length 520;
Best Local Similarity 68.5%; Pred. No. 2.2e-126;
Matches 342; Conservative 57; Mismatches 97; Indels 3; Gaps 2;

Qy 1 AIGPVASLVANAPVSPDGFURDAIVNGVSPSLITGKGRFQLNVDVTLTHSMKLS 60
Dy 23 AIGPVTLTISGVDSPDGFTRAAVLAVGPPGLITGKGNQINIDLSNETMLKS 82
Qy 61 TSIHWHGFQAGTNAGDPFAVNCPTASGHSFLYDEHVPDQAGTFWYHSHLSQYCDGL 120
Dy 83 TSIHWHGFQAGTNAGDPAFVNCQPIATGNSFLYDTATDQAGTFWYHSHLSQYCDGL 142
Qy 121 RGPFWVDPKDPHASRYDVDDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSAST 180
Dy 143 RGPWVYDPSDADLYDVDDDETHITLSDWYHTAASLGAAPFGSDSTLNGLSRAGG 202
Qy 181 PTAALAVINVOHGKRYRFLVSIISCDPNYTSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Dy 203 DSTDLAVITVEQGRYRMRLLSLSCDPNYVFSIDGHNMTIADAVNHEPLTVDSIQIYA 262
Qy 241 AQRYSFVLNANOTVGNVWRANPNFVGFAGGINSAILRYQGPAPVAEPTTQTSVIPL 300
Dy 263 GQRYSEVLTAQDDINDVIRALPAGTTSFDGGINSAIRLYSGASEVDPTTETTSVLPL 322
Qy 301 IETNLHPLARMVPVSPGVDKALNLAFFNGTFFINNATFTPTVPVLLQILSGAQ 360
Dy 323 DEANLVPLDSPAAQDPNIGGVADYALNLDNFNCTGFINDVSFVTPVLLILSGTT 382
Qy 361 TAQDLLPAGSVYPLPAHSTIETITLPATAL-APGAPHPHLHGAFVAVRSAGSTYVND 419
Dy 383 SAADLLPSGLSFAVPSNTSISPTATNAPAGAPHPHLHGHTFSIVRTAGSDTNEVN 442
Qy 420 PIERDVYSTGTPAAGDNVTIFQDNDGCPWFLHCHIDPHLDAGPAIYFAEDVADVKAANP 479
Dy 443 PVRDQVNTGT--VGDNVTIFRTDNGCPWFLHCHIDPHLEAGFAIYFSEDTADVSNTT 500
Qy 480 VPKASDLCPIYDGLSEAN 498
Dy 501 PSTAWEDLCPTYNALDSSD 519

RESULT 9
LACI_PLEOS
ID LACI_PLEOS STANDARD; PRT; 529 AA.
AC Q12729;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Laccase 1 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN POX1.
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
[1]
SEQUENCE FROM N.A.
RN STRAIN=Florida; TISSUE=Mycelium;
RX MEDLINE=95314294; PubMed=7793961;
RA Giardina P., Canio R., Martirani L., Marzullo L., Palmieri G.,
RA Sanna G.;
RT "Cloning and sequencing of a laccase gene from the lignin-degrading
RT basidiomycete Pleurotus ostreatus."
RL Appl. Environ. Microbiol. 61:2408-2413(1995).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLY).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
CC H2O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
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Db 382 PVLQLSGATTAALLPSGSIYEANKWEISIP--ALAVGGPHPHLHGHTFDVRS 439
Qy 410 AGSTTYNYNDPIFRDVSSTPAAGDNVTIRFOTNPGGFWFLCHIDFHLDAAGFAIVPAE 469
Db 440 AGSTTYNEDTPARDVVTGTD-ANDNTVIRVTNPGGFWFLCHIDHWHLEIGLAVVPAE 498
Qy 470 DVAADVKAANVPKAWSDLCPIYDGLSEANQ 499
Db 499 DVTSITAP---PAAWDDLCPYDALSDSK 525

RESULT 10
LAC2_PLEOS STANDARD: PRT; 533 AA.
AC Q12739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (diphenol oxidase).
GN POX2.
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE FROM N.A., CARBOHYDRATE-LINKAGE SITE, AND MASS SPECTROMETRY.
RC TISSUE=Mycelium;
RX MEDLINE=96184523; PubMed=8654395;
RA Giardina P., Aurilia V., Cannio R., Marzullo L., Amoresano A.,
RA Siciliano R., Pucci P., Sannia G.;
RA Cannio R., Sannia G.;
RT "Stability and activity of a phenol oxidase from the ligninolytic
RT fungus Pleurotus ostreatus.";
RL Eur. J. Biochem. 235:508-515(1996).
RP CHARACTERIZATION.
RC STRAIN=Florida; TISSUE=Mycelium;
RX MEDLINE=93356991; PubMed=7763931;
RA Palmieri G., Giardina P., Marzullo L., Desiderio B., Nitti G.,
RA Cannio R., Sannia G.;
RT "Stability and activity of a phenol oxidase from the ligninolytic
RT fungus Pleurotus ostreatus.";
RL Appl. Microbiol. Biotechnol. 39:632-636(1993).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: N-GLYCOSYLATED AT ASN-467 BY A HIGH-MANNOSE STRUCTURE WITH A
CC VARYING NUMBER OF MANNOSE RESIDUES. THERE EXIST NO FURTHER POST-
CC TRANSLATIONAL MODIFICATION.
CC -!- MISCELLANEOUS: POX2 ISOZYME IS THE MOST ABUNDANT LACCASE OF
CC P. OSTREATUS UNDER VARIOUS GROWTH CONDITIONS.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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or send an email to license@isb-sib.ch).
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DB EMBL; 249075; CAA88895.1; -
DB EMBL; 234848; CAA84357.1; -
DB HSSP; P37064; IAOZ.
DB InterPro; IPR001117; Cu-oxidase.
DB InterPro; IPR002355; MultiCu_oxidse2.
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DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 533 LACCASE 2.
FT DOMAIN 25 171 PLASTOCYANIN-LIKE 1.
FT DOMAIN 173 336 PLASTOCYANIN-LIKE 2.
FT DOMAIN 382 501 PLASTOCYANIN-LIKE 3.
FT METAL 98 98 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 100 100 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 145 145 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 427 427 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 432 432 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 483 483 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 484 484 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 485 485 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 489 489 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 467 467 N-LINKED (GLCNAC... ) (HIGH MANNOSE).
SQ SEQUENCE 533 AA; 56766 MW; 7233C41D47E19AE6 CRC64;

Query Match 65.3%; Score 1743.5; DB 1; Length 533;
Best Local Similarity 64.8%; Pred. No. 3.le-117;
Matches 330; Conservative 49; Mismatches 109; Indels 21; Gaps 7;

Qy 1 AIGPVASIVVANAPVSPDGFRLDAIVVNGV-----VPSPLITCKKGRQLNVV 49
Db 24 AIGPAGNIVIVNEDVSPDGFARSAVSVPATDTPATASIPVLVKNKGDNFQNVV 83
Qy 50 DPLTNHSLKSTSIHWHGFFQAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWH 109
Db 84 NQLSDTHLKTTSIHWHGFFQAGSSWADGPAFVTCQPVASGDSFLYNFVNPQAGTFWH 143
Qy 110 SHLSTQYCDGLRGPFVYDVKDPHASRYDVNDNESVITLTDWYHTAARLGRPRPLGADAT 169
Db 144 SHLSTQYCDGLRGPFVYDVKDPHASRYDVNDNESVITLTDWYHTAARLGRPRPLGADAT 169
Qy 170 LINGGRASSTPAALAVINVOHGRYRFLVSCDPNVTESIDGHNLTVIEVDGINSQ 229
Db 203 LINGGRAGSTPAALAVINVOHGRYRFLVSCDPNVTESIDGHNLTVIEVDGINSQ 229
Qy 230 PLVDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFGAGGINSAILRQGGAPVAP 289
Db 263 PITVDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFGAGGINSAILRQGGAPVAP 289
Qy 290 TTTQTTSVPIETNLHPLARMPVPGSPGVDKALNLAFFNFGTNF--FTNNATFTPP 347
Db 323 TTTSTST-PLLETNLVPLENPGAPGPPVPGGADININLAMAFAFTTFTLTINGVPFLPP 381
Qy 348 TVPVLQLLSGAOTADLLPAGSVYPLPAHSTIETLTPATALPAGPHPHLGHAFV 407
Db 382 TAPVLQLLSGAOTADLLPAGSVYPLPAHSTIETLTPATALPAGPHPHLGHAFV 407
Qy 408 RSAGSTTYNYNDPIFRDVSSTPAAGDNVTIRFOTNPGGFWFLCHIDFHLDAAGFAIV 467
Db 440 RSAGSTTYNYNDPIFRDVSSTPAAGDNVTIRFOTNPGGFWFLCHIDFHLDAAGFAIV 467
Qy 468 REDVADVKAANVPKAWSDLCPIYDGLSE 496
Db 499 AEDVTSITAP---PAAWDDLCPYDALSD 524

RESULT 11
LAC1_PHLRA
ID LAC1_PHLRA STANDARD: PRT; 548 AA.
AC Q01679;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

DE Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Ligninolytic phenoloxidase).
GN LAC.
OS Phlebia radiata (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Phlebia.
OX NCBI_TaxID=5308;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 6458;
RX MEDLINE=92065223; PubMed=1955850;
RA Saohelmo M., Niku-Paavola M.L., Knowles J.K.;
RT Isolation and structural analysis of the laccase gene from the
RT lignin-degrading fungus *Phlebia radiata*.
RL J. Gen. Microbiol. 137:1537-1544(1991).
CC -!- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN
CC DEGRADATION.
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52134; CAA36379.1; -;
DR EMBL; A20705; CAA01513.1; -;
DR PIR; S18746; S18746.
DR HSSP; P37064; IASQ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 548
FT DOMAIN 22 148
FT DOMAIN 160 304
FT DOMAIN 373 496
FT METAL 85 85
FT METAL 87 87
FT METAL 130 130
FT METAL 132 132
FT METAL 418 418
FT METAL 421 421
FT METAL 423 423
FT METAL 473 473
FT METAL 474 474
FT METAL 475 475
FT METAL 479 479
FT METAL 484 484
FT CARBOHYD 75 75
FT CARBOHYD 352 352
FT CARBOHYD 402 402
FT CARBOHYD 457 457
SQ SEQUENCE 548 AA; 58601 MW; 3445A757E3C56B2 CRC64;
Query Match 64.3%; Score 1716; DB 1; Length 548;
Best Local Similarity 69.4%; Pred. No. 3e-115;
Matches 326; Conservative 42; Mismatches 92; Indels 10; Gaps 6;
QY 1 AIGFVASLVVAPSPDGLRDAIVVGVPSFLITGKGRFQLNVDTLTHNSMLKS 60

Db 22 SIGPVTDFHVNAAVSPDGFSGQAVLAEGVFGPLIAGNKGDNFQINVIDELTNATMLKT 81
QY 61 TSHHWCFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSFYQYCDGL 120
Db 82 TTHHWCFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSFYQYCDGL 141
QY 121 RGPVYVDPKDPHASRYDVNDNESTVITLTDMYHTAARLGRPRFPLGADATLINGLGR--SA 178
Db 142 RGFVYVDPADPYLDQYDVDDSTVITLADWYHTAARLGRSPFP-AADTTILINGLGRGEA 200
QY 179 STTAALAVINVQHKRYRFLYSICDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQI 238
Db 201 GCPVSDLAIVSVTKGRYRFLYSICDSFFTSIDGHSLNVEVDATNHLQPLTVDELTI 260
QY 239 FAQRYSFVLNANQTVGNVYVRANPNFG-TVGAGGINSAILRYQGAPEPTTQTSV 297
Db 261 YAGORYSFILTAODVDVNIWRANPGIGITGAGGINSAILRYDGDVVEPTTQATSP 320
QY 298 IPIETNLHPLARMPVPGSPTPGVDKALNAFNFNGTN--FFTNATFTPTTPVVLQI 355
Db 321 VVLSNLAPLTNAAPGLPEVGVLDLALNFNLTFDGPSLKFOINGVTFVPTVPVLQI 380
QY 356 LSGAQTADLLPAGSVYPLPAHSTIETITPATALAPCAPHPHLHGHAFVAVRSAGTTY 415
Db 381 LSGAQAADLLPGSVYALPSNATIELSLPAGAL--GGPHPHLHGHTFSVVRPAGTTY 438
QY 416 NYNDPTFRDVGTTGTPAAGNVNIRFQTDNPGPWFHLCHIDFHLDAAGAI 465
Db 439 NYNVPQDVVVSIGN--TGDNVITREDTNNPGPWFHLCHIDHLEAALPL 486
RESULT 12
LAC3_TRAVI STANDARD; PRT; 473 AA.
ID LAC3_TRAVI
AC Q99049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase 3 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC3
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=47662;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97128774; PubMed=89773314;
RA Xaver D.S., Gollightly E.J.;
RT "Cloning and characterization of three laccase genes from the
RT white-rot basidiomycete Trametes villosa: genomic organization of the
RT laccase gene family."
RL Gene 181:95-102(1996).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----

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CC EMBL; L78076; AAB47733.1; -
DR HSSP; P37064; IAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 473 LACASE 3.
FT DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
FT DOMAIN 160 298 PLASTOCYANIN-LIKE 2.
FT DOMAIN 365 444 PLASTOCYANIN-LIKE 3.
FT METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 410 410 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 413 413 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 415 415 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 426 426 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 427 427 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 428 428 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 432 432 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 433 432 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 470 470 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 473 AA; 51923 MW; B29FDE944DCE547 CRC64;
```

Query Match 60.2%; Score 1606.5; DB 1; Length 473;
Best Local Similarity 61.9%; Pred. No. 1.6e-107;
Matches 305; Conservative 34; Mismatches 105; Indels 49; Gaps 4;

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Qy 1 AIGPVASLVANAPVPGFLRDAIVNGVVPSPILITGKGDGRFOLNVVDITLNISM LKS 60
Db 22 SIGPVTELDIVNKVITAPDGVARDVITAGGTFPGPLITGKGNFRINVDKLVNQTMLTS 81
Qy 61 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSEFLYDFHVPQAGTFVYHSHLSTOYCDGL 120
Db 82 TTIHWHGMEQHTNWADGPAFVTCQPIITGDDFLYFNRVVDGTGYVYHSHLALQYCDGL 141
Qy 121 RGFVYVDPKDPHASYRDVNDNESTVITITDWTYHTAARLGRPRPLGADATLNGLSRST 180
Db 142 RGPLVIYDPHPQAVLYDVDDESTVITITDWTYHTAARLGRPRPLGADATLNGLSRST 196
Qy 181 PTAALAVINVOHGKRYRRLYSISCDPNYTSIDGHNLTVEVDGINSOPLVDVSIOLFA 240
Db 197 PTADLAVIEVHGKRYRRLYSISCDPNYTSIDGHNLTVEVDGINSOPLVDVSIOLFA 256
Qy 241 AQRYSFVLNANQTVGNVYWRANPN-FGTGVFAGGINSAILRYQGAPEAEPTTQTSVIP 299
Db 257 AQRYSFVLNANQVNNYWRANPNRANTTGFANGINSAILRYKGAPEAEPTTQTSVIP 316
Qy 300 LIETNLHPLARMPVPGSTPGGVKALMLANFNCTNFFINNTPTPTVPVLLQILSGA 359
Db 317 LWETDLHLPLTPRAGLPFGKGVVDHMLNLTFFNGSEFFINDAPVPTPTVPVLLQILNGT 376
Qy 360 QTAQDLLPAGSVYPLPAHSTTEITLPTALAPGAPFHLHAFVAVRSAGSTTYND 419
Db 377 LDANDLLPPGSVYNLPDSTIELSPGG--VTGGPHPLHG----- 416
Qy 420 PIFRDVSTGTGAAGDNTYIRFQTDNPGFWFLHCHIDFHLDAFVAIVFAEDVADYKAAP 479
Db 417 -----TDNPGFWFLHCHIDFHLDAFVAIVFAEDVADYKAAP 453
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Qy 480 VPKAWSDLQPIYD 492
Db 454 VPEDWNKLCPTFD 466

RESULT 13
LAC2_AGABI STANDARD; PRT; 520 AA.
AC Q12542;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase II precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC2.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=D649;
RX MEDLINE=93367392; PubMed=8360614;
RA Perry C.R., Smith M., Britnell C.H., Wood D.A., Thurston C.F.;
RT "Identification of two laccase genes in the cultivated mushroom
   Agaricus bisporus.";
RL J. Gen. Microbiol. 139:1209-1218(1993).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC -!- PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC -!- CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC -!- 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L10663; AAB17035.1; -
DR HSSP; P37064; IASQ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat; Multigene family.
FT SIGNAL 1 19
FT CHAIN 20 520 LACCASE II.
FT DOMAIN 21 145 PLASTOCYANIN-LIKE 1.
FT DOMAIN 157 305 PLASTOCYANIN-LIKE 2.
FT DOMAIN 375 488 PLASTOCYANIN-LIKE 3.
FT METAL 82 82 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 84 84 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 127 127 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 417 417 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 422 422 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 470 470 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 471 471 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 476 476 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 7 7 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 108 108 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 520 AA; 57822 MW; EF100145F0A697AA CRC64;

Query Match 45.7%; Score 1219.5; DB 1; Length 520;
Best Local Similarity 49.0%; Pred. No. 7.8e-80;
Matches 251; Conservative 70; Mismatches 140; Indels 51; Gaps 15;

QY 10 VANAPVSPDGLRDAIVVGVSPPLITGKGRFQNLNVVDTLTNHSMLKSTSIHHGFF 69
Db 28 LVNRLAPDGFERTVTVINGEFTGLVQVNGKSVRIPVANKLTSFMRSSVSIHHGFF 87
QY 70 QAGTNWADGPAFVNCQPIASGSHFLYDFHVPDQAGTGFYHSHLSYQCDGLRGPFVYDPP 129
Db 88 QARTSGDGFPAFVNCQPPNTTTFYFVSAEQSGTGFYHSHLSYQCDGLRGAFVYDPP 147
QY 130 KDPHASRYVDNVESTVITLTDWYHTAA--RLGPRFPLG----ADATLINGLGRSASTPTA 183
Db 148 RDLRLHLYDVDDSTVITLAEWYHILAPDATNEFFSSGIIIPVDSGLNGKRGNGGLPT 207
QY 184 ALAVINQHGKRYRFLVSVISCDPNYTFSDHNLTVIEVDGINSOPLLDVDSIQIFAAR 243
Db 208 PFVAVNVRGKRYRLVIAISCRFFTFSDVNDHSLVFEADGVDEHPVQVONVDIYAAAR 267
QY 244 YSFVLNANQTVGNVWRA-----NPNEGTGVFAGGINSAILRYOGAPVAEPTTQT 294
Db 268 VSVILHANQPIDNWIAPMTGGNDRPNLNI-----SLTALILRYHGAREVETTVN- 321
QY 295 TSVIP---LIETNLHPLARMPVPGSPGPGVDK--ALMLAFNFGTFFINATFTPTTV 349
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RESULT 14

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LACI_LAGABI STANDARD; PRT; 520 AA.
AC Q12541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase I precursor (EC 1.10.3.2) (benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC1.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=D649; TISSUE=Mycelium;
RX MEDLINE=93367392; PubMed=8360614;
RA Perry C.R., Smith M., Britnell C.H., Wood D.A., Thurston C.F.;
RT Identification of two laccase genes in the cultivated mushroom
RT Agaricus bisporus.
RL J. Gen. Microbiol. 139:1209-1218(1993).
CC -I- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -I- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
```

```
CC -I- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L10664; AAC18877.1; -.
DR HSP; P37064; IAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat; Multigene family.
FT SIGNAL 1..19
FT CHAIN 20..520 LACCASE I.
FT DOMAIN 21..145 PLASTOCYANIN-LIKE 1.
FT DOMAIN 157..305 PLASTOCYANIN-LIKE 2.
FT DOMAIN 375..488 PLASTOCYANIN-LIKE 3.
FT METAL 82..82 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 84..84 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 127..127 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129..129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 417..417 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 420..420 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 422..422 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 470..470 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 471..471 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 472..472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 476..476 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ?..? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 108..108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239..239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299..299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454..454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 492..492 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 520 AA; 58099 MW; 943DB3F23297B891 CRC64;

Query Match 44.7%; Score 1192.5; DB 1; Length 520;
Best Local Similarity 48.1%; Pred. No. 6.6e-78;
Matches 245; Conservative 71; Mismatches 148; Indels 45; Gaps 14;

QY 10 VANAPVSPDGLRDAIVVGVSPPLITGKGRFQNLNVVDTLTNHSMLKSTSIHHGFF 69
Db 28 LVNRLAPDGFERTVTVINGEFTGLVQVNGKSVRIPVANKLTSFMRSSVSIHHGFF 87
QY 70 QAGTNWADGPAFVNCQPIASGSHFLYDFHVPDQAGTGFYHSHLSYQCDGLRGPFVYDPP 129
Db 88 QARTSGDGFPAFVNCQPPNTTTFYFVSAEQSGTGFYHSHLSYQCDGLRGAFVYDPP 147
QY 130 KDPHASRYVDNVESTVITLTDWYHTAA--RLGPRFPLG----ADATLINGLGRSASTPTA 183
Db 148 RDLRLHLYDVDDSTVITLAEWYHILAPDATNEFFSSGIIIPVDSGLNGKRGNGGLPT 207
QY 184 ALAVINQHGKRYRFLVSVISCDPNYTFSDHNLTVIEVDGINSOPLLDVDSIQIFAAR 243
Db 208 PFVAVNVRGKRYRLVIAISCRFFTFSDVNDHSLVFEADGVDEHPVQVONVDIYAAAR 267
QY 244 YSFVLNANQTVGNVWRA-----NPNEGTGVFAGGINSAILRYOGAPVAEPTTQT 294
Db 268 VSVILHANQPIDNWIAPMTGGNDRPNLNI-----SLTALILRYHGAREVETTVN- 321
QY 295 TSVIP---LIETNLHPLARMPVPGSPGPGVDK--ALMLAFNFGTFFINATFTPTTV 349
```


Db 322 ---VPGKLLDQEMHPI-RQEGPKGLGDPDPKHITLNLIA-OPNAPFEDINGISYISPTV 376
QY 350 PVLQILISGTAQADLLPAGSVPLPAHSHTIETLPATLAPAGPHFHLHGHAFAVRS 409
Db 377 PVLQILISGAKRPEDVLPSEIIFVPKNSLIEYNIP-----GEGA-HPFHLHGHNFDVYLA 431
QY 410 AGSTYNYNDPIFRDVTSTGTPAAGDNVIRFOTDNPFGPWFHLCHIDFHLDAAGFAIVFAE 469
Db 432 SNDDTFNFKNPPRDVY----PINGGNTYFRFTDNPFCANFLHCHIDHLEAGLAIIVFAE 487
QY 470 DVADVKAANP-----VPKAWSDLCPYDGL 494
Db 488 APED-NVSGPQSQTTPQDMLDCLPEYNAI 515
RESULT 15
LAC4_THACU STANDARD; PRT; 531 AA.
AC Q02081;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC4.
OS Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae;
OC mitosporic Ceratobasidiaceae; Rhizoctonia.
OX NCBI_Taxid=107832;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=RS22;
RX MEDLINE=96171523; PubMed=8598061;
RA Wahleithner J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J.,
RA Halkier T., Kauppinen S., Pedersen A., Schneider P.;
RT "The identification and characterization of four laccases from the
RT plant pathogenic fungus Rhizoctonia solani";
RL Curr. Genet. 29:395-403(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 7.
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COPACITOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: IN MYCELIA, AT A HIGHER LEVEL THAN LCC1, LCC2
CC AND LCC3.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC
CC EMBL: Z54277; CAA91042.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002335; MultiCu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; FALSE NEG.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
Lignin degradation; Multigene family; Polymorphism.
FT SIGNAL 1 19
FT CHAIN 20 531 LACCASE 4.
FT DOMAIN 23 146 PLASTOCYANIN-LIKE 1.

FT DOMAIN 158 315 PLASTOCYANIN-LIKE 2.
FT DOMAIN 384 507 PLASTOCYANIN-LIKE 3.
FT METAL 83 83 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 85 85 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 128 128 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 427 427 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 432 432 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 480 480 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 481 481 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 484 484 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 42 42 P -> S.
FT VARIANT 119 119 H -> R.
FT VARIANT 246 246 R -> S.
FT VARIANT 256 256 P -> L.
FT VARIANT 261 261 P -> A.
SQ SEQUENCE 531 AA; 57545 MW; 737339803F75AB19 CRC64;
Query Match 40.4%; Score 1077; DB 1; Length 531;
Best Local Similarity 47.3%; Pred. No. 1.2e-69;
Matches 223; Conservative 56; Mismatches 152; Indels 40; Gaps 10;
QY 10 VANAPVSPDGLRDAIVVNGVSPSLITGKGRFQNLVVDVTLNHSMLKSTSHHGFF 69
Db 29 IKVNVAPDCFORPIVSVNGLVPGTLTANKGDTLRINVTNQLTDPMSRRATTHHGLF 88
QY 70 QAGTNWADGPAFVNCQPIASGHSLFDHFVDPQAGTFWYHSHLSQVCDGLRGPVYDP 129
Db 89 QATTADRDGPAFVTCQPIAQNLSYIEPLHGTGTWYHAHLASQVVDGLRGLVYDP 148
QY 130 KDPHASRYDVNDNESTVITLTDWYHT-----AARLGPFPGLADATFLINGLG 175
Db 149 NDPKSKRYDVDDASTVVMLEDWYHTPAPVLEKQMFNTNTALLSP-----VPDSGLINGKG 204
QY 176 RSASTPFAALAVINQHGKRYRFLVSIQDPNTFSDGHNLTVIEVDGINSOPLLVDS 235
Db 205 RYVGGPAPRPSVINVKRGKRYRLRVINASAIGSTFSEIGHRLTVIEADGPHQPLVD 264
QY 236 IQIFAAQRYSEVLNANOTGVNVRANPNFTGTFAGGINS-----ATLRQOGAPVAPETT 291
Db 265 FQIYAGQRYSVIVEANOTAAVYIRAPMTVAGAGTNANLDPTNVFVLTHTGAPNAEPTT 324
QY 292 TQTTSV-IPLIETNLHPLARMPVPGSPPTGGVDKALNLFNFGTN----FFINNAFTTP 346
Db 325 EQGSAIGTALVEENLHALINPGAPGSGAP--ADVSLNLAIGRSTVDGILRFTFNKVEA 382
QY 347 PTPVPLIQL-SCAQTADLLPAGSVPLPAHSHTIETLPATLAPAGPHFHLHGHAFA 405
Db 383 PSLPTLKIILANNASNDADFTPNHHTIIVLPNKKVI-----GAQHHRGADPHIHLGHVFD 437
QY 406 VRSAGSTTVNYNDPIFRDVTSTGTPAAGDNVIRFOTDNPFGPWFHLCHID 456
Db 438 IVKSLGGTP-NYVNPFRDVRVG-----GTGVVLRFRKADNPGPWFVHCHID 483

Search completed: December 14, 2002, 08:26:12
Job time : 31 secs

XX Claim 9; Page 17-19; 34pp; English.

PS The Trametes versicolor laccase gene can be used to create transgenic

CC plants which produce laccase at levels of about 0.01% or higher of the

CC total soluble protein of the plant. The transgenic plants may be used

CC for the large scale production of laccase enzymes. Laccase is mainly

CC used in the paper and pulp industry for breaking down lignin.

CC Conversely, laccase is also involved in lignin biosynthesis and the

CC formation of lignin polymers. It is therefore useful as a biological

CC adhesive for gluing wood (e.g. in the production of plywood, oriented

CC strand board, particle board and medium density fiberboard). Laccase

CC may also be used for catalyzing the oxidation of compounds such as

CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is

CC also used as a marker enzyme in enzyme immunoassays, for the oxidation

CC of steroids and the synthesis of vinblastine (a cytostatic compound

CC used in treating malignant diseases).

XX

SQ Sequence 1500 BP; 275 A; 551 C; 402 G; 272 T; 0 other;

Query Match 100.0%; Score 1500; DB 21; Length 1500;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGGCGGTGGGAGCCTCGTCGCGGAACGCCCGCTCGCCGCGAGGGTTC 60

DB 1 GCCATCGGGCGGTGGGAGCCTCGTCGCGGAACGCCCGCTCGCCGCGAGGGTTC 60

QY 61 CTTCCGGATGCCATCGTGGTCAACGGGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG 120

DB 61 CTTCCGGATGCCATCGTGGTCAACGGGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG 120

QY 121 GGAGACCGCTTCCAGCTCAACGCTCGTGGACACCTTGACCAACACAGCATGCTCAAGTCC 180

DB 121 GGAGACCGCTTCCAGCTCAACGCTCGTGGACACCTTGACCAACACAGCATGCTCAAGTCC 180

QY 181 ACTAGTATCACTGGACGGCTTCTCCAGGAGGACCAACTGGGAGACGACCGCGG 240

DB 181 ACTAGTATCACTGGACGGCTTCTCCAGGAGGACCAACTGGGAGACGACCGCGG 240

QY 241 TTGCTCAACAGTGCCTATTGCTTCGGGCACTTCTTCTGACGACTTCCATGTGCC 300

DB 241 TTGCTCAACAGTGCCTATTGCTTCGGGCACTTCTTCTGACGACTTCCATGTGCC 300

QY 301 GACAGGACGAGAACTGCTGGTACCAAGTCTGTCTACGCAATACTGTGACGGGCTG 360

DB 301 GACAGGACGAGAACTGCTGGTACCAAGTCTGTCTACGCAATACTGTGACGGGCTG 360

QY 361 CGAGGACCGTTCGCTGTGACGACCCCAAGATCCGACGCGCCGCTACGATGTTGAC 420

DB 361 CGAGGACCGTTCGCTGTGACGACCCCAAGATCCGACGCGCCGCTACGATGTTGAC 420

QY 421 AACGAGACGAGGTTCATCAGCTTGACCGACTGGTACCACACCGCTGCCGCGTCCG 480

DB 421 AACGAGACGAGGTTCATCAGCTTGACCGACTGGTACCACACCGCTGCCGCGTCCG 480

QY 481 AGGTTCCTCACTCGGCGGAGCGCACGCTCATCAATGGTCTTGGGCGGTGGGCTCCACT 540

DB 481 AGGTTCCTCACTCGGCGGAGCGCACGCTCATCAATGGTCTTGGGCGGTGGGCTCCACT 540

QY 541 CCCACCGCGGCTTGTGTGATCAAGTCCAGTCCAGCAGGAAAGCGCTACCGTTCGCTC 600

DB 541 CCCACCGCGGCTTGTGTGATCAAGTCCAGTCCAGCAGGAAAGCGCTACCGTTCGCTC 600

QY 601 GTTTCGATCTCGTCGACCGGACTACACGTTTCAGATCCAGCGGCAATCTCACCGTCC 660

DB 601 GTTTCGATCTCGTCGACCGGACTACACGTTTCAGATCCAGCGGCAATCTCACCGTCC 660

QY 661 ATCAGGTTCAGCGGTATCAACAGCGCCCTCTCTCTGCTGACTCTATCCAGATCTTCGCC 720

DB 661 ATCAGGTTCAGCGGTATCAACAGCGCCCTCTCTCTGCTGACTCTATCCAGATCTTCGCC 720

QY 721 GCGGAGCGCTACTCTTTGTTGATGCGAACCAACCGTTCGCGCAACTACTGGGTCCGC 780

DB 721 GCGCAGCGCTACTCTTTGTTGAATGCAACCAACCGTTCGCAACTACTGGGTCCGC 780

QY 781 GCGAACCCGAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCATCTCTCGCG 840

DB 781 GCGAACCCGAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCATCTCTCGCG 840

QY 841 TACCAAGGCGACAGTTCGCGAGCCCACTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

DB 841 TACCAAGGCGACAGTTCGCGAGCCCACTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

QY 901 ATGAGACGAACTTCGACCCCTTCGCTCGCATGCTGCTGGCAGCCCGACACCGCGG 960

DB 901 ATGAGACGAACTTCGACCCCTTCGCTCGCATGCTGCTGGCAGCCCGACACCGCGG 960

QY 961 GCGTTCGACAAGGCGTCAACCTCGGTTTAACTTCAACGCGACCAACTTCTTCATCAAC 1020

DB 961 GCGTTCGACAAGGCGTCAACCTCGGTTTAACTTCAACGCGACCAACTTCTTCATCAAC 1020

QY 1021 AACGCGACTTTCACGCGCGCGACCGTCCCGGTACTCTCCAGATTCTGAGCGGTGCGCAG 1080

DB 1021 AACGCGACTTTCACGCGCGCGACCGTCCCGGTACTCTCCAGATTCTGAGCGGTGCGCAG 1080

QY 1081 ACCGCAACACCTGCTCCCTGCGAGGCTCTGTACCCGCTCCCGCCGCTCCACCATC 1140

DB 1081 ACCGCAACACCTGCTCCCTGCGAGGCTCTGTACCCGCTCCCGCCGCTCCACCATC 1140

QY 1141 GAGATCAGCTGCCCGCGACCGCTTGGCCCGGGTGCACGCGACCGCTTCCACCTGCAC 1200

DB 1141 GAGATCAGCTGCCCGCGACCGCTTGGCCCGGGTGCACGCGACCGCTTCCACCTGCAC 1200

QY 1201 GGTACGCGCTTCCGCGTTCGTCAGCGCGGGGAGCACACGTAATACTACAAGACCGG 1260

DB 1201 GGTACGCGCTTCCGCGTTCGTCAGCGCGGGGAGCACACGTAATACTACAAGACCGG 1260

QY 1261 ATCTTCGCGACGTCGTGACGACGGGACCGCGCGGGGGGAGCACACGTCAGATCCG 1320

DB 1261 ATCTTCGCGACGTCGTGACGACGGGACCGCGCGGGGGGAGCACACGTCAGATCCG 1320

QY 1321 TTCAGACGACAAACCCCGCGGTGTTCTCCACTGCCACATCGACTTCCACCTGCAC 1380

DB 1321 TTCAGACGACAAACCCCGCGGTGTTCTCCACTGCCACATCGACTTCCACCTGCAC 1380

QY 1381 GCGGGCTTCGCGATCGTGGTTCGAGAGGACGTTGCGGACGTGAAGCGGGAACCCGGT 1440

DB 1381 GCGGGCTTCGCGATCGTGGTTCGAGAGGACGTTGCGGACGTGAAGCGGGAACCCGGT 1440

QY 1441 CCGAAGCGGTGGTTCGCGACCTGTCGCCGATCTACGACGGGTGACGAGGCTAACCACTGA 1500

DB 1441 CCGAAGCGGTGGTTCGCGACCTGTCGCCGATCTACGACGGGTGACGAGGCTAACCACTGA 1500

RESULT 2

ABA92910

ID ABA92910 standard; cDNA; 1500 BP.

XX

XX ABA92910;

XX AC AC

XX

DT 09-APR-2002 (first entry)

XX

DE Trametes versicolor laccase I gene.

XX

XX Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;

KW copper; metal cofactor; gene; plant; ds.

XX

OS Trametes versicolor.

XX

XX Key Location/Qualifiers

FF CDS 1..1500

FF

FF /*tag= a

FF /partial

FF /product= "laccase I"

FF /note= "no start codon given"

[illegible]

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RESULT 3
AAAT15599
ID AAAT15599 standard; DNA; 2880 BP.
XX
AC AAAT15599;
XX
DT 07-APR-1996 (first entry)
XX
DE Laccase-LCC2 gene.
XX
KW Laccase-LCC2; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pBSY19;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ss.
XX
OS Polyporus pinsitus.
OS Trametes villosa.
XX
FH Key
FH CDS Location/Qualifiers
FT 364..2492
FT /*tag= a
FT /product= Laccase-LCC2
FT /note= "EC-1.10.3.2"
FT sig_peptide
FT 364..423
FT /*tag= b
FT 364..543
FT /*tag= c
FT 544..592
FT /*tag= d
FT 593..661
FT /*tag= e
FT 662..715
FT /*tag= f
FT 716..835
FT /*tag= g
FT 836..899
FT /*tag= h
FT 900..1013
FT /*tag= i
FT 1014..1066
FT /*tag= j
FT 1067..1132
FT /*tag= k
FT 1133..1187
FT /*tag= l
FT 1188..1283
FT /*tag= m
FT 1284..1343
FT /*tag= n
FT 1344..1498
FT /*tag= o
FT 1499..1553
FT /*tag= p
FT 1554..1751
FT /*tag= q
FT 1752..1815
FT /*tag= r
FT 1816..1872
FT /*tag= s
FT 1873..1928
FT /*tag= t
FT 1929..2135
FT /*tag= u
FT 2136..2195
FT /*tag= v
FT 2196..2492
FT /*tag= w
XX
PN WO9600290-A1.
XX

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PD 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
XX 15-MAY-1995; 95US-0441147.
PR 24-JUN-1994; 94US-0265534.
XX
XX (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO-NORDISK AS.
XX
XX Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
PI WPI; 1996-068874/07.
XX P-PSDB; AAR90722.
DR
XX DNA constructs for expression of Polyporus laccase enzymes - for use
FT in e.g. lignin manipulation, juice mfr., phenol polymerisation and
FT phenol resin prodn
XX
XX Claim 5; Page 62-65; 137pp; English.
XX
XX The sequence encodes laccase-LCC2 (pi 5.95) from Polyporus pinsitus
CC (Trametes villosa). Polymerase chain reaction (PCR) amplification of
CC P. pinsitus cDNA using primers 3331 (AAAT15603) and 3332 (AAAT15604) gives
CC a 1500 bp fragment, which is joined to a signal peptide sequence
CC from a 43-kDa cellulase using primer PHD433 (AAAT15605) and a pUC
CC forward primer in PCR. Clones are expressed in Aspergillus oryzae,
CC and a cDNA probe is obtained and used to screen a P. pinsitus
CC genomic library in Escherichia coli DH5-alpha, giving plasmid
CC pDSY19 (23GEN), with a 4-kb HindIII insert (NRRL B-21266).
CC Screening also results in isolation of LCC1 (AAAT15598) and LCC3-LCC5
CC (AAAT15600-T15602), which encode different laccases produced by P.
CC pinsitus. The laccases may be used to polymerise lignin or
CC lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
CC precursors, in hair dye compositions, or to polymerise or oxidise a
CC phenolic or aniline compound. These new laccases are well-expressed
CC in Aspergillus spp. (with vector integration in the genome), in
CC contrast to previous basidiomycete laccases, which give low yields
CC of recombinant enzyme.
XX
SQ Sequence 2880 BP; 547 A; 908 C; 793 G; 632 T; 0 other;
Query Match 16.4%; Score 246; DB 17; Length 2880;
Best Local Similarity 99.7%; Pred. No. 6.4e-109;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1204 CACGCCCTTCGGGTCGTTCCGACGGGGAGCACCACGTATACACACCGGATC 1263
DB 1204 CACGCCCTTCGGGTCGTTCCGACGGGGAGCACCACGTATACACACCGGATC 1263
DB 2196 CACGCCCTTCGGGTCGTTCCGACGGGGAGCACCACGTATACACACCGGATC 2255
QY 1264 TTCGCGGACGTCGTGAGCAGCGGGACGCCGCCGGGGAGCAGTCACGTCGCTTC 1323
DB 1264 TTCGCGGACGTCGTGAGCAGCGGGACGCCGCCGGGGAGCAGTCACGTCGCTTC 1323
DB 2256 TTCGCGGACGTCGTGAGCAGCGGGACGCCGCCGGGGAGCAGTCACGTCGCTTC 2315
QY 1324 CAGACGGACACCCCGGGCCGTGTTCTCCACTGCCACATCGACTTCACCTCGACGG 1383
DB 1324 CAGACGGACACCCCGGGCCGTGTTCTCCACTGCCACATCGACTTCACCTCGACGG 1383
DB 2316 CAGACGGACACCCCGGGCCGTGTTCTCCACTGCCACATCGACTTCACCTCGACGG 2375
QY 1384 GGCTTCGGGATCGTTCGACGAGGACGTTGCGGACGTGAGCGGCGGACCGGTTCCG 1443
DB 1384 GGCTTCGGGATCGTTCGACGAGGACGTTGCGGACGTGAGCGGCGGACCGGTTCCG 1443
DB 2376 GGCTTCGGGATCGTTCGACGAGGACGTTGCGGACGTGAGCGGCGGACCGGTTCCG 2435
QY 1444 AAGGCGTGTGCGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTAACAGTGA 1500
DB 1444 AAGGCGTGTGCGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTAACAGTGA 1500
DB 2436 AAGGCGTGTGCGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTAACAGTGA 2492
XX
RESULT 4
AAZ23937
ID AAZ23937 standard; DNA; 7986 BP.
XX
XX AC AAZ23937;
XX

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DT 27-JAN-2000 (first entry)
XX T. versicolor laccase I DNA.
DE Filamentous fungus; hydrolytic enzyme; cellulase; hemicellulase;
KW lipase; oxidoreductase; lignin peroxidase; mangan peroxidase;
KW cellobiose-chinon oxidoreductase; cellobiose-oxidase; laccase I; ss.
XX Trametes versicolor.
OS
XX WO9951757-A1.
PN 14-OCT-1999.
XX 01-APR-1999; 99WO-EP02252.
XX 02-APR-1998; 98DE-1014853.
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
PA Pfaller R, Hessing J, Van Den Hondel C, Van Gorcom R;
PI WPI; 1999-633742/54.
XX An expression system for the production of proteins in filamentous
PT fungi.
XX
XX Claim 8; Page 50-53; 67pp; German.
XX This invention describes a novel expression system for the production
CC of a protein in a filamentous fungus which comprises a Trametes or
CC Polyporus host organism, a DNA vector containing a positive selection
CC marker and a DNA vector containing a gene of interest controlled by an
CC active genetic regulation element in the host organism. The fungi are
CC useful for the production of hydrolytic enzymes, e.g. cellulases,
CC hemicellulase and lipases or oxidoreductases, e.g. lignin peroxidase,
CC mangan peroxidase, laccase, cellobiose-chinon oxidoreductase or
CC cellobiose-oxidase. This sequence represents the laccase I nucleic acid
CC sequence isolated from Trametes versicolor.
XX
SQ Sequence 7986 BP; 1698 A; 2404 C; 2107 G; 1777 T; 0 other;
Query Match 10.5%; Score 158; DB 20; Length 7986;
Best Local Similarity 100.0%; Pred. No. 2.3e-66;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 584 GCTACCGCTTCGCTCTCGTTTCGATCTCGTGGACCCGAACTACAGTTTCAGCATCGAGC 643
DB 2170 GCTACCGCTTCGCTCTCGTTTCGATCTCGTGGACCCGAACTACAGTTTCAGCATCGAGC 2229
QY 644 GGCACAATCTGACCGTCATCGAGTTCGAGGTATCAACAGCCAGCCTCTCCTTGTGCACT 703
DB 2230 GGCACAATCTGACCGTCATCGAGTTCGAGGTATCAACAGCCAGCCTCTCCTTGTGCACT 2289
QY 704 CTATCCAGATCTTGGCGCGCAGCGCTACTCTCTTGTG 741
DB 2290 CTATCCAGATCTTGGCGCGCAGCGCTACTCTTGTG 2327
RESULT 5
ABL60268
ID ABL60268 standard; cDNA; 1563 BP.
XX
XX ABL60268;
XX
XX 23-AUG-2002 (first entry)
XX Trametes versicolor Laccase III encoding cDNA SEQ ID NO 25.
DE
XX Fungi; Thal; Ctal; copper-dependent secreted protein; copper; laccase;
KW Trametes ATR1 homologue; copper transporting Atpase; gene; ss.
XX
XX Trametes versicolor.
OS
```

```
XX Key Location/Qualifiers
FH 1..1563
FT /*tag= a
FT /product= "Laccase Iii"
XX DE10046932-A1.
XX 16-MAY-2002.
XX 21-SEP-2000; 2000DE-1046932.
XX 21-SEP-2000; 2000DE-1046932.
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX Marbach-Ringhandt K, Pfaller R, Uldschmid A;
XX WPI; 2002-445163/48.
XX P-PSDB; ABE77510.
XX Expression system for increased production of copper-dependent enzymes,
PT particularly laccase, includes the gene for a copper homeostasis
PT protein.
XX
XX Example 9; Page 46-48; 58pp; German.
XX The invention relates to an expression system (A) that provides increased
CC expression of copper-dependent secreted proteins (I) in eukaryotic cells
CC comprises a gene (II) that encodes (I) and at least one cooper
CC homeostasis gene (III). (A) is used to express enzymes, especially
CC laccase, that require copper as co-factor. (III) transports copper to the
CC secretory pathway so its overexpression leads to increased yields of (I).
CC The present sequence is that of the Trametes versicolor Laccase III
CC encoding polynucleotide of the invention.
XX
SQ Sequence 1563 BP; 271 A; 603 C; 384 G; 305 T; 0 other;
Query Match 2.5%; Score 38; DB 24; Length 1563;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1379
DB 1405 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1442
RESULT 6
AAT15598
ID AAT15598 standard; DNA; 2418 BP.
XX
XX AAT15598;
AC
XX 07-APR-1996 (first entry)
DT Laccase-LCC1 gene.
DE
XX Laccase-LCC1; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pdsy18;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ds.
XX
XX Polyporus pinsitus.
OS Trametes villosa.
XX
XX Key Location/Qualifiers
FH CAAT_signal 19..22
FT /*tag= a
FT TATA_signal 129..134
FT /*tag= b
FT CDS 231..2223
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FT FT /*tag= c
FT FT /product= Laccase-LCC1
FT FT /note= "EC-1.10.3.2"
FT FT 231..293
FT FT /*tag= d
FT FT 231..413
FT FT /*tag= e
FT FT 414..464
FT FT /*tag= f
FT FT 465..533
FT FT /*tag= g
FT FT 534..589
FT FT /*tag= h
FT FT 590..709
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FT FT 710..764
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FT FT 765..878
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FT FT 879..934
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FT FT /*tag= m
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FT FT /*tag= n
FT FT 1051..1146
FT FT /*tag= o
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FT FT /*tag= p
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FT FT /*tag= q
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FT FT /*tag= r
FT FT 1411..1610
FT FT /*tag= s
FT FT 1609..1662
FT FT /*tag= t
FT FT 1663..2223
FT FT /*tag= u
XX PN WO9600290-A1.
XX PD 04-JAN-1996.
XX PF 15-JUN-1995; 95WO-US07536.
XX PR 15-MAY-1995; 95US-0441147.
XX PR 24-JUN-1994; 94US-0265534.
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX WPI; 1996-068874/07.
XX P-PSDB; AAR90721.
XX PT DNA constructs for expression of Polyporus laccase enzymes - for use
XX PT in e.g. lignin manipulation, juice mfr., phenol polymerisation and
XX PT phenol resin prodn
XX PS Claim 3; Page 57-60; 137pp; English.
XX The sequence encodes laccase-LCC1 (pi 4.49) from Polyporus pinsitus
XX (Trametes villosa). Polymerase chain reaction (PCR) amplification of
XX P. pinsitus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
XX a 1500 bp fragment, which is joined to a signal peptide sequence
XX from a 43-kDa cellulase using primer pHD433 (AAT15605) and a pUC
XX forward primer in PCR. Clones are expressed in Aspergillus oryzae,
XX and a cDNA probe is obtained and used to screen a P. pinsitus
XX genomic library in Escherichia coli XL1-Blue, giving plasmid pDSY18
XX (21GEN) with an 8.0-kb BamHI insert (NRRL B-21265). Screening also
XX results in isolation of LCC2-LCC5 (AAT15599-T15602), which encode
```

```
CC different laccases produced by P. pinsutus. The laccases may be
CC used to polymerise lignin or lignosulphonates, to depolymerise
CC kraft pulp, to oxidise dyes or precursors, in hair dye
CC compositions, or to polymerise or oxidise a phenolic or aniline
CC compound. These new laccases are well-expressed in Aspergillus
CC spp. (with vector integration in the genome), in contrast to
CC previous basidiomycete laccases, which give low yields of
CC recombinant enzyme.
XX SQ Sequence 2418 BP; 465 A; 799 C; 589 G; 565 T; 0 other;
Query Match 2.5%; Score 38; DB 17; Length 2418;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
DB 2065 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2102
RESULT 7
AAZ23938
ID AAZ23938 standard; DNA; 5762 BP.
XX AC AAZ23938;
XX 27-JAN-2000 (first entry)
XX DE T. versicolor laccase III DNA.
XX KW Filamentous fungus; hydrolytic enzyme; cellulase; hemicellulase;
XX KW lipase; oxidoreductase; lignin peroxidase; mangan peroxidase;
XX KW cellobiose-chinon oxidoreductase; cellobiose-oxidase; laccase III; ss.
XX OS Trametes versicolor.
XX PN WO9951757-A1.
XX PD 14-OCT-1999.
XX PF 01-APR-1999; 99WO-EP02252.
XX PR 02-APR-1998; 98DE-1014853.
XX PA (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX PI Pfaller R, Hessing J, Van Den Hondel C, Van Gorcom R;
XX WPI; 1999-633742/54.
XX An expression system for the production of proteins in filamentous
XX fungi -
XX Claim 8; Page 53-55; 67pp; German.
XX This invention describes a novel expression system for the production
XX of a protein in a filamentous fungus which comprises a Trametes or
XX Polyporus host organism, a DNA vector containing a positive selection
XX marker and a DNA vector containing a gene of interest controlled by an
XX active genetic regulation element in the host organism. The fungi are
XX usefull for the production of hydrolytic enzymes, e.g. cellulases,
XX hemicellulase and lipases or oxidoreductases, e.g. lignin peroxidase,
XX mangan peroxidase, laccase, cellobiose-chinon oxidoreductase or
XX cellobiose-oxidase. This sequence represents the laccase III nucleic acid
XX sequence isolated from Trametes versicolor.
XX SQ Sequence 5762 BP; 1113 A; 1781 C; 1644 G; 1224 T; 0 other;
Query Match 2.5%; Score 38; DB 20; Length 5762;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
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Db 2387 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2424
|||||

RESULT 8
AAQ03367
ID AAQ03367 standard; DNA; 1497 BP.
XX AC AAQ03367;
XX DT 18-AUG-1990 (first entry)
XX DE Phenol oxidase (PO) gene.
XX KW Phenol oxidase (PO) gene; enzyme.
XX PN JP02005877-A.
XX PD 10-JAN-1990.
XX PF 16-JUN-1988; 88JP-0149103.
XX PR 16-JUN-1988; 88JP-0149103.
XX PA (OJIP) OJI PAPER KK.
XX DR WPI; 1990-053914/08.
XX DR P-PSDB; AAR05279.
XX PT Phenol oxidase gene - used for biological pulping, etc.
XX PS Page 812-813; Fig 2; 14pp; Japanese.
XX CC It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridizing to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.
XX SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 9
AAQ03571
ID AAQ03571 standard; DNA; 1497 BP.
XX AC AAQ03571;
XX DT 03-FEB-1991 (first entry)
XX DE Sequence encoding phenol oxidase (PO).
XX KW Paper pulping; ds.
XX PN JP02027986-A.
XX PD 30-JAN-1990.
XX PF 15-JUL-1988; 88JP-0175236.
XX PR 15-JUL-1988; 88JP-0175236.
XX PA (OJIP) OJI PAPER KK.
XX DR WPI; 1990-323326/43.

DR P-PSDB; AAR07068.
XX New phenol oxidase gene - has DNA encoding specified sequence of
PT 499 aminoacid(s)
XX Claim 4; Fig 2; 15pp; Japanese.
XX PO is useful in biological paper pulping and bleaching.
XX SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 10
AAQ03572
ID AAQ03572 standard; DNA; 1497 BP.
XX AC AAQ03572;
XX DT 03-FEB-1991 (first entry)
XX DE Sequence encoding phenol oxidase (PO).
XX KW Paper pulping; ds.
XX PN JP02027986-A.
XX PD 30-JAN-1990.
XX PF 15-JUL-1988; 88JP-0175236.
XX PR 15-JUL-1988; 88JP-0175236.
XX PA (OJIP) OJI PAPER KK.
XX DR WPI; 1990-323326/43.
XX DR P-PSDB; AAR07069.

New phenol oxidase gene - has DNA encoding specified sequence of
499 aminoacid(s)
Claim 5; Fig 3; 15pp; Japanese.
PO is useful in biological paper pulping and bleaching.
SQ Sequence 1497 BP; 272 A; 536 C; 377 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 11
AAQ03366
ID AAQ03366 standard; DNA; 2049 BP.
XX AC AAQ03366;
XX DT 18-AUG-1990 (first entry)
XX DE Phenol oxidase (PO) gene with introns.

Phenol oxidase (PO) gene; enzyme.

XX Key Location/Qualifiers
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FT /*tag= a
FT /note="exon 1"
FT intron 121..176
FT /*tag= b
FT /note="intron 1"
FT exon 177..245
FT /*tag= c
FT /note="exon 2"
FT intron 246..297
FT /*tag= d
FT /note="intron 2"
FT exon 298..418
FT /*tag= e
FT /note="exon 3"
FT intron 419..480
FT /*tag= f
FT /note="intron 3"
FT exon 481..594
FT /*tag= g
FT /note="exon 4"
FT intron 595..648
FT /*tag= h
FT /note="intron 4"
FT exon 649..712
FT /*tag= i
FT /note="exon 5"
FT intron 713..772
FT /*tag= j
FT /note="intron 5"
FT exon 773..868
FT /*tag= k
FT /note="exon 6"
FT intron 869..923
FT /*tag= l
FT /note="intron 6"
FT exon 924..1080
FT /*tag= m
FT /note="exon 7"
FT intron 1081..1136
FT /*tag= n
FT /note="intron 7"
FT exon 1137..1334
FT /*tag= o
FT /note="exon 8"
FT intron 1335..1390
FT /*tag= p
FT /note="intron 8"
FT exon 1391..1447
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FT /note="exon 9"
FT intron 1447..1497
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FT /note="intron 9"
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FT /note="exon 11"
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PN
XX 10-JAN-1990.
PD
XX 16-JUN-1988; 88JP-0149102.
PF
XX

PR 16-JUN-1988; 88JP-0149102.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-053913/08.
DR P-PSDB; AAR05279.
XX
PT Phenol oxidase gene - used for biological pulping, etc.
XX
PS Page 799-800; Fig 2; 12pp; Japanese.
XX
CC It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93366 ligated with vector DNA.
XX
SQ Sequence 2049 BP; 386 A; 681 C; 499 G; 483 T; 0 other;
Query Match 2.3%; Score 35; DB 11; Length 2049;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGTTCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 1894 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 1928
RESULT 12
AAQ03573
ID AAQ03573 standard; DNA; 2049 BP.
XX
AC AAQ03573;
XX
DT 15-AUG-1990 (first entry)
DE
XX Phenol oxidase gene.
KW Phenol oxidase; biological pulping; bleaching; paper; ss.
XX
FH Key Location/Qualifiers
FT exon 1..121
FT /*tag= a
FT exon 177..245
FT /*tag= b
FT exon 298..418
FT /*tag= c
FT exon 481..594
FT /*tag= d
FT exon 649..712
FT /*tag= e
FT exon 773..868
FT /*tag= f
FT exon 924..1080
FT /*tag= g
FT exon 1137..1334
FT /*tag= h
FT exon 1391..1447
FT /*tag= i
FT exon 1498..1704
FT /*tag= j
FT exon 1756..2049
FT /*tag= k
FT exon 773..868
FT /*tag= l
XX JF02027985-A.
PN
XX 30-JAN-1990.
PD
XX 15-JUL-1988; 88JP-0175235.
PF
XX 15-JUL-1988; 88JP-0175235.
PR

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XX (OJIP ) OJI PAPER KK.
XX WPI; 1990-072975/10.
DR P-PSDB; AAR05668.
XX
XX DNA code for phenol oxidase gene - of specified
PT amino acid sequence is separated by introns.
XX
XX Claim 4; Page 2; 13pp; Japanese.
XX
XX Phenol oxidase encoded by the gene is used in biological
CC pulping and bleaching of paper.
XX
XX Sequence 2049 BP; 386 A; 681 C; 499 G; 483 T; 0 other;
SQ
Query Match 2.3%; Score 35; DB 11; Length 2049;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTCTCCACTGCCACATCGACTTCCACCT 1376
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 1894 CCGTGGTCTCCACTGCCACATCGACTTCCACCT 1928
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 13
AAT15602
ID AAT15602 standard; DNA; 2925 BP.
XX
XX AAT15602;
XX
XX 07-APR-1996 (first entry)
XX
XX Laccase-LCC5 gene.
XX
XX Laccase-LCC5; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pDSY22;
KW plasmid pDSY23; lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ds.
XX
XX Polyporus pinsitus.
OS Trametes villosa.
XX
XX
XX Key Location/Qualifiers
FH CAAT_signal 278..282
FT /*tag= a
FT TATA_signal 438..442
FT /*tag= b
FT CDS 545..2810
FT /*tag= c
FT /*product= Laccase-LCC5
FT /*note= "EC-1.10.3.2"
FT sig_peptide 545..613
FT /*tag= d
FT exon 545..733
FT /*tag= e
FT intron 734..808
FT /*tag= f
FT exon 809..877
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FT intron 878..932
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FT exon 933..1052
FT /*tag= i
FT intron 1053..1106
FT /*tag= j
FT exon 1107..1220
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FT intron 1221..1272
FT /*tag= l
FT exon 1273..1338

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FT exon 2749..2810
FT /*tag= {
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XX WO9600290-A1.
XX
XX 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
XX 15-MAY-1995; 95US-0441147.
PR 24-JUN-1994; 94US-0265534.
XX
XX (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO NORDISK AS.
XX
XX Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
XX WPI; 1996-068874/07.
DR P-PSDB; AAR90725.
XX
XX DNA constructs for expression of Polyporus laccase enzymes - for use
in e.g. lignin manipulation, juice mfr., phenol polymerisation and
phenol resin prodn
XX
XX Claim 11; Page 78-81; 137pp; English.
XX
XX The sequence encodes laccase-LCC5 (pI 4.07) from Polyporus pinsitus
(Trametes villosa). Polymerase chain reaction (PCR) amplification of
P. pinsutus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
a 1500 bp fragment, which is joined to a signal peptide sequence
from a 43-kDa cellulase using primer PHD433 (AAT15605) and a pUC
forward primer in PCR. Clones are expressed in Aspergillus oryzae,
and a cDNA probe is obtained and used to screen a P. pinsutus
genomic library in Escherichia coli DH5-alpha, giving plasmid
pDSY22 (41GEN), with a 3.0-kb EcoRI insert (NRRL B-21263) and
plasmid pDSY23 (41GEN), with a 4.5-kb MluI insert containing part of
the pDSY22 insert and 5'-sequences. Screening also results in
isolation of LCC1-LCC4 (AAT15598-15601) which encode different
laccases produced by P. pinsutus. The laccases may be used to
polymerise lignin or lignosulphonates, to depolymerise Kraft pulp,
to oxidise dyes or precursors, in hair dye compositions, or to
polymerise or oxidise a phenolic or aniline compound. These new
laccases are well-expressed in Aspergillus spp. (with vector
integration in the genome), in contrast to previous basidiomycete
laccases, which give low yields of recombinant enzyme.
XX

```

171020VYH AC

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:48:01 : Search time 2136 Seconds
(without alignments)
11373.235 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgccgcgtggcgag.....tgagcgaggtcaaccagtga 1500

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	23	1.5	794	17 CNS03GCZ	AL242828 Tetraodon
2	22	1.5	523	11 AY105245	AY105245 Zea mays
3	22	1.5	530	17 BH774999	BH774999 fzmbo11f0
4	22	1.5	583	10 AW231821	AW231821 687042B12
c 5	21	1.4	264	9 AI102246	AI102246 EST211535
c 6	21	1.4	322	9 AI231258	AI231258 EST227946

c 7	21	1.4	341	9 AI412412	AI412412 EST240711
c 8	21	1.4	371	9 AA899112	AA899112 UI-R-E0-C
c 9	21	1.4	374	9 AI409646	AI409646 EST237938
c 10	21	1.4	381	9 AI234086	AI234086 EST230774
c 11	21	1.4	392	9 AI179240	AI179240 EST222931
c 12	21	1.4	397	9 AI103006	AI103006 EST212295
c 13	21	1.4	399	10 AW141507	AW141507 EST291561
c 14	21	1.4	401	10 BE110478	BE110478 UI-R-BJL-
c 15	21	1.4	401	12 BG371835	BG371835 UI-R-CV0-
c 16	21	1.4	401	13 BM389935	BM389935 UI-R-CN1-
c 17	21	1.4	402	12 BF544071	BF544071 UI-R-E0-C
c 18	21	1.4	404	9 AA944766	AA944766 EST200265
c 19	21	1.4	410	9 AI179051	AI179051 EST222734
c 20	21	1.4	418	9 AI179789	AI179789 EST223518
c 21	21	1.4	423	9 AI1010901	AI1010901 EST205352
c 22	21	1.4	429	9 AI1011109	AI1011109 EST210398
c 23	21	1.4	431	12 BG669875	BG669875 DRNALE07
c 24	21	1.4	435	9 AA851745	AA851745 EST194513
c 25	21	1.4	436	9 AI229927	AI229927 EST226632
c 26	21	1.4	440	9 AI008888	AI008888 EST203339
c 27	21	1.4	443	9 AI169426	AI169426 EST215277
c 28	21	1.4	446	12 BG670125	BG670125 DRNAQA11
c 29	21	1.4	449	9 AI229900	AI229900 EST226595
c 30	21	1.4	451	9 AI233932	AI233932 EST230620
c 31	21	1.4	452	9 AI407646	AI407646 EST235936
c 32	21	1.4	453	9 AI229540	AI229540 EST226235
c 33	21	1.4	455	9 AI231104	AI231104 EST227792
c 34	21	1.4	456	9 AI102729	AI102729 EST212018
c 35	21	1.4	457	9 AI145993	AI145993 UI-R-BT0-
c 36	21	1.4	462	9 AA859998	AA859998 UI-R-E0-C
c 37	21	1.4	462	9 AA900005	AA900005 UI-R-E0-C
c 38	21	1.4	463	9 AI180279	AI180279 EST224032
c 39	21	1.4	469	9 AI177784	AI177784 EST221437
c 40	21	1.4	471	9 AA944292	AA944292 EST199791
c 41	21	1.4	471	9 AI103271	AI103271 EST212560
c 42	21	1.4	471	9 AI230644	AI230644 EST227339
c 43	21	1.4	471	9 AI406329	AI406329 EST234615
c 44	21	1.4	490	9 AI177851	AI177851 EST221499
c 45	21	1.4	492	9 AI013026	AI013026 EST207477

ALIGNMENTS

RESULT 1	CNS03GCZ	794 bp	DNA	linear	GSS 17-MAY-2000
LOCUS	Tetraodon nigroviridis genome survey sequence PUC-ori end of clone 024C10 of library G from Tetraodon nigroviridis, genomic survey sequence.				
DEFINITION	AL242828				
ACCESSION	AL242828.1 GI:7963597				
VERSION	GSS: genome survey sequence.				
KEYWORDS	Tetraodon nigroviridis.				
SOURCE	Tetraodon nigroviridis.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.				
REFERENCE	1 (bases 1 to 794)				
AUTHORS	Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 794)				
AUTHORS	Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
JOURNAL	Unpublished				

REFERENCE 3 (bases 1 to 794)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_lib="G"
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BASE COUNT 178 a 183 c 196 g 229 t 8 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1386 CTTCCGATCGTGTTCGACAGG 1408
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Db 560 CTTCCGATCGTGTTCGACAGG 538

RESULT 2
AY105245
LOCUS 523 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0098568 mRNA sequence.
ACCESSION AY105245
VERSION AY105245.1 GI:21208323
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 523)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
Coe,E.C.
2 (bases 1 to 523)
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1..523
/organism="Zea mays"
/db_xref="MaizeDB:635644"
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/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 77 a 203 c 139 g 104 t
ORIGIN
Query Match 1.5%; Score 22; DB 11; Length 523;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCCGTCGCCCGACGGCTTCC 61
|||||

Db 167 CCCGTCGCCCGACGGCTTCC 188
|||||

RESULT 3
BH774999
LOCUS 530 bp DNA linear GSS 28-MAR-2002
DEFINITION fzmbo11f004h06f0 fzmbo filtered library Zea mays genomic clone fzmbo11f004h06 5', DNA sequence.

ACCESSION BH774999
VERSION BH774999.1 GI:19777116
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 530)
Budiman,M.A., Freese,R.G., Bedell,J.A., Nunberg,A.N. and Lakey,N.D.
Generethresher methylation filtered genomic sequences from maize Unpublished (2002)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fzmbo11f004 row: h column: 06
Seq primer: M13 forward
Class: shotgun
High quality sequence stop: 530.
Location/Qualifiers
1..530
/organism="Zea mays"
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/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells."

BASE COUNT 96 a 195 c 124 g 115 t
ORIGIN
Query Match 1.5%; Score 22; DB 17; Length 530;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCCGTCGCCCGACGGCTTCC 61
|||||

Db 272 CCCGTCGCCCGACGGCTTCC 293
|||||

RESULT 4
AW231821
LOCUS 583 bp mRNA linear EST 30-MAR-2000
DEFINITION 687042B12.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.

ACCESSION AW231821
VERSION AW231821.1 GI:6564199
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 583)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 687042 row: B column: 12.
Location/Qualifiers

FEATURES

source
1. .583
/organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
/tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLF"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
; Site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
2 others

BASE COUNT 85 a 218 c 175 g 103 t
ORIGIN
Query Match 1.5%; Score 22; DB 10; Length 583;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CCCGTCGCGCGACGGCTCC 61
|||||
Db 29 CCCGTCGCGCGACGGCTCC 50

RESULT 5

AI102246/c
LOCUS AI102246 264 bp mRNA linear EST 31-JAN-1999
DEFINITION EST211535 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBC806 3' end, mRNA sequence.

ACCESSION AI102246
VERSION AI102246.1 GI:3707047
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 264)
AUTHORS Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.

TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index

JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
source
1. .264
/organism="Rattus sp."
/db_xref="ATCC (inhost):2024496"
/db_xref="taxon:10118"
/clone="RBC806"
/clone_lib="Normalized rat brain, Bento Soares"

BASE COUNT 72 a 55 c 71 g 66 t
ORIGIN
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

Query Match 1.4%; Score 21; DB 9; Length 264;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 6

AI231258/c

LOCUS AI231258 322 bp mRNA linear EST 31-JAN-1999
DEFINITION EST27946 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMDE78 3' end, mRNA sequence.

ACCESSION AI231258
VERSION AI231258.1 GI:3815138
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 322)
AUTHORS Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.

TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index

JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
source
1. .322
/organism="Rattus sp."
/db_xref="ATCC (inhost):2038867"
/db_xref="taxon:10118"
/clone="REMDE78"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"

BASE COUNT 85 a 59 c 80 g 88 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 261 CGGCACCAACTTCTTCATCAA 241

ACCESSION AI412412
VERSION AI412412.1 GI:4255916
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

```

Rattus..
1 (bases 1 to 341)
REFERENCE
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..341
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RBRDU52"
/clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 87 a 74 c 85 g 95 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 341;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 8
AA899112/c
LOCUS AA899112 371 bp mRNA linear EST 05-FEB-1999
DEFINITION UI-R-E0-cw-d-11-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone
UI-R-E0-cw-d-11-0-UI 3' similar to gi|55891|emb|X54737|RNCBETAR Rat
mRNA for the cystatin beta, mRNA sequence.
ACCESSION AA899112
VERSION AA899112.1 GI:4231612
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 371)
REFERENCE
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT On Apr 7, 1998 this sequence version replaced gi:3034466.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult 8-day-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics
Seq primer: M13 Forward.
Location/Qualifiers
1..371
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"

```

```

/clone="UI-R-E0-cw-d-11-0-UI"
/clone_lib="UI-R-E0"
/dev_stage="embryonic"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73b-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
the mixture."
BASE COUNT 103 a 72 c 85 g 111 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 352 CGGCACCAACTTCTTCATCAA 332

RESULT 9
AI409646/c
LOCUS AI409646 374 bp mRNA linear EST 09-FEB-1999
DEFINITION EST237538 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVEN88 3' end, mRNA sequence.
ACCESSION AI409646
VERSION AI409646.1 GI:4253150
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 374)
REFERENCE
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..374
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="ROVEN88"
/clone_lib="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 110 a 70 c 92 g 102 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 10
AI234086/c
LOCUS AI234086 381 bp mRNA linear EST 31-JAN-1999

```



```

DEFINITION EST230774 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
ACCESSION RLUC095.3' end, mRNA sequence.
VERSION AI234086
KEYWORDS EST.
SOURCE AI234086.1 GI:3817966
ORGANISM Rattus sp.
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 381)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Other ESTs: TC62051
          Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..381
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2039745"
              /db_xref="taxon:10118"
              /clone="RLUC095"
              /clone_lib="Normalized rat lung, Bento Soares"
              /note="Organ: lung; Vector: pT7T3Pac; Site_1: EcoRI;
              Site_2: NotI"

BASE COUNT 114 a 73 c 91 g 103 t
ORIGIN

Query Match 1.4%; Score 21; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 11
AI179240/c
LOCUS
DEFINITION EST222931 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
ACCESSION RSPCE16.3' end, mRNA sequence.
VERSION AI179240
KEYWORDS EST.
SOURCE AI179240.1 GI:3729878
ORGANISM Rattus sp.
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 392)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..392
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2039745"
              /db_xref="taxon:10118"
              /clone="RSPCE16"
              /clone_lib="Normalized rat spleen, Bento Soares"
              /dev_stage="embryo 8, 12, 18 dpc"
              /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"

BASE COUNT 117 a 76 c 93 g 111 t
ORIGIN

Query Match 1.4%; Score 21; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 13
AW141507
LOCUS
DEFINITION EST291561 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
          RIBX21.5' end similar to cystatin beta, mRNA sequence.
ACCESSION AW141507
VERSION AW141507.1 GI:6161305
  
```

```

/organism="Rattus sp."
/db_xref="ATCC (inhost):2033816"
/db_xref="taxon:10118"
/clone="RSPCE16"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 30 a 91 c 105 g 106 t
ORIGIN

Query Match 1.4%; Score 21; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 12
AI103006/c
LOCUS
DEFINITION EST212295 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
ACCESSION REMBW03.3' end, mRNA sequence.
VERSION AI103006
KEYWORDS EST.
SOURCE AI103006.1 GI:3704801
ORGANISM Rattus sp.
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 397)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..397
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2023069"
              /db_xref="taxon:10118"
              /clone="REMBW03"
              /clone_lib="Normalized rat embryo, Bento Soares"
              /dev_stage="embryo 8, 12, 18 dpc"
              /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"

BASE COUNT 117 a 76 c 93 g 111 t
ORIGIN

Query Match 1.4%; Score 21; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 13
AW141507
LOCUS
DEFINITION EST291561 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
          RIBX21.5' end similar to cystatin beta, mRNA sequence.
ACCESSION AW141507
VERSION AW141507.1 GI:6161305
  
```

KEYWORDS
SOURCE
ORGANISM

EST.
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 399)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.

TITLE

Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat

JOURNAL

Gene Index

COMMENT

Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For information availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (<http://www.tigr.org/tdb/rqi/rqi.html>). To order a clone
contact the ATCC (<http://www.atcc.org/atcc.html>).
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers
1..399
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGIBX21"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 110 a 104 c 94 g 91 t

Query Match

Best Local Similarity 1.4%; Score 21; DB 10; Length 399;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

999 CGGCACCAACTTCTTCATCAA 1019

Db

150 CGGCACCAACTTCTTCATCAA 170

RESULT 14

BE110478/c
LOCUS

DEFINITION

BE110478 401 bp mRNA linear EST 13-JUN-2000
UI-R-BJ1-auc-e-03-0-UI-s1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-auc-e-03-0-UI 3', mRNA sequence.

ACCESSION

BE110478

VERSION

BE110478.1 GI:8502583

KEYWORDS

EST.

SOURCE

Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 401)

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dt track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site

FEATURES

source

Location/Qualifiers
1..401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10118"
/clone="UI-R-BJ1-auc-e-03-0-UI"
/clone_lib="UI-R-BJ1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73b-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
library is a subtracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-BJ1
TAG_TISSUE=AV canal at 16.5 dpc
TAG_SEQ=GAACC"
BASE COUNT 115 a 72 c 92 g 122 t

Query Match

Best Local Similarity 1.4%; Score 21; DB 10; Length 401;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

999 CGGCACCAACTTCTTCATCAA 1019

Db

354 CGGCACCAACTTCTTCATCAA 334

RESULT 15

BG371835/c
LOCUS

DEFINITION

BG371835 401 bp mRNA linear EST 09-MAR-2001
UI-R-CV0-bri-h-07-0-UI-s1 UI-R-CV0 Rattus norvegicus cDNA clone
UI-R-CV0-bri-h-07-0-UI 3', mRNA sequence.

ACCESSION

BG371835

VERSION

BG371835.1 GI:13268372

KEYWORDS

EST.

SOURCE

Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 401)

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dt track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dt track served to verify it as a clone from the
non-normalized rat eye library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through

and the oligo-dt track served to identify it as a clone from the
normalized AV canal at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward

POLYA-Yes.

Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes

FEATURES
source

Location/Qualifiers
1..401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CV0-bri-h-07-0-UI"
/clone_lib="UI-R-CV0"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-CV0
library is a non-normalized library constructed from rat
eye tissue. For a detailed description of the library from
which this clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-CV0
TAG_TISSUE=rat eye
TAG_SEQ=CAGCC"

BASE COUNT 115 a 73 c 91 g 122 t
ORIGIN

Query Match 1.4%; Score 21; DB 12; Length 401;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCACTTCTTCATCAA 1019
|||||
DB 355 CGGCACCACTTCTTCATCAA 335

Search completed: December 14, 2002, 08:22:39
Job time : 2155 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 08:26:17 ; Search time 21 seconds
(without alignments)
395.929 Million cell updates/sec

Title: US-09-786-960-2
Perfect score: 2669
Sequence: 1 AIGPVASLVVANAPVSPDGF.....VPRAWSDLCPYDGLSEANQ 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2656	99.5	499	10	US-09-732-350-3
2	2201	82.5	499	10	US-09-732-350-2
3	1716	64.3	548	10	US-09-732-350-4
4	1533	57.4	539	10	US-09-732-350-1
5	1178.5	44.2	529	10	US-09-732-350-5
6	1000	37.5	599	10	US-09-732-350-6
7	930.5	34.9	572	10	US-09-732-350-7
8	884.5	33.1	575	10	US-09-732-350-8
9	577	21.6	616	10	US-09-732-350-9
10	575	21.5	573	10	US-09-732-350-10
11	512.5	19.2	564	9	US-09-942-160-12
12	207	7.8	572	9	US-09-942-185-4
13	206	7.7	568	12	US-10-080-233-4
14	176.5	6.6	627	12	US-10-080-210-7
15	176	6.6	627	12	US-09-338-723A-4
16	176	6.6	627	12	US-10-080-210-4
17	171.5	6.4	594	10	US-09-338-723A-2
18	171.5	6.4	594	12	US-10-080-210-2
19	171.5	6.4	594	12	US-10-080-233-2

20	170	6.4	583	9	US-09-942-185-2	Sequence 2, Appli
21	123	4.6	655	9	US-09-712-363-207	Sequence 207, App
22	111.5	4.2	3472	9	US-10-027-806-4	Sequence 4, Appli
23	109	4.1	772	10	US-09-884-441-388	Sequence 388, App
24	109	4.1	833	10	US-09-884-441-389	Sequence 389, App
25	109	4.1	914	10	US-09-778-320-206	Sequence 206, App
26	109	4.1	914	10	US-09-910-689-206	Sequence 206, App
27	109	4.1	914	10	US-09-884-441-312	Sequence 312, App
28	109	4.1	914	10	US-09-884-441-478	Sequence 478, App
29	109	4.1	914	12	US-10-010-742-206	Sequence 206, App
30	109	4.1	1148	10	US-09-884-441-458	Sequence 458, App
31	109	4.1	1148	10	US-09-884-441-479	Sequence 479, App
32	109	4.1	1156	10	US-09-884-441-459	Sequence 459, App
33	106	4.0	5795	10	US-09-815-242-12610	Sequence 12610, A
34	100.5	3.8	513	10	US-09-833-745-47	Sequence 47, Appl
35	100.5	3.8	513	10	US-09-833-745-48	Sequence 48, Appl
36	100	3.7	482	9	US-09-992-598-513	Sequence 513, App
37	100	3.7	482	9	US-09-989-293A-513	Sequence 513, App
38	100	3.7	482	9	US-10-066-500-63	Sequence 63, Appl
39	100	3.7	482	10	US-09-989-722-513	Sequence 513, App
40	100	3.7	482	10	US-09-989-723-513	Sequence 513, App
41	100	3.7	482	10	US-09-989-279-513	Sequence 513, App
42	100	3.7	482	10	US-09-989-727-513	Sequence 513, App
43	100	3.7	482	10	US-09-989-731-513	Sequence 513, App
44	100	3.7	482	10	US-09-989-732-513	Sequence 513, App
45	100	3.7	482	10	US-09-991-073-513	Sequence 513, App

ALIGNMENTS

RESULT 1
US-09-732-350-3
; Sequence 3, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,350
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/032,315
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rorek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,350
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-4

Query Match 64.3%; Score 1716; DB 10; Length 548;
Best Local Similarity 69.4%; Pred. No. 1.4e-135;
Matches 326; Conservative 42; Mismatches 92; Indels 10; Gaps 6;

QY 1 AIGPVASLVANAPVSPGFLRDAIVNGVVPSPITKGGDRFQNLNVVDLTNHSMLKS 60
DB 22 SIGPVTDFHIVNAAPVSPGFSRQVLAEGVFPGLIAGNKGDFQINVIDELTNATMLKT 81
QY 61 TSIHHGFFOAGTNWADGPAFVNQCPIASGHSFLYDFHVDPQAGTFWYHSHLSYQCDGL 120
DB 82 TTIHHGFFOAGTNWADGPAFVNQCPIASGHSFLYDFHVDPQAGTFWYHSHLSYQCDGL 141
QY 121 RGFVVYDPKPHASRYDVNDSVTITLTDWYHTAARLGPRLGADATLNLGLGR--SA 178
DB 142 RGFVVYDPAADYLDQYDVBDDSVTITLADWYHTAARLGSPPF-AADTTLLNGLRGCEA 200
QY 179 STPTAALAVINVQHKRYRFRVLSISCDPNYTFSDGHNLTVEVDGINSQPLLVDSIQI 238
DB 201 GCPVSDLAIVSTGKRYRFRVLSISCDPFSTFSDGHSNLTVEVDGINSQPLLVDSIQI 260
QY 239 FAAQRYSFVLNANQVGNVWRANPNFG--TVGFAGGINSAILRYOGAPVAEPTTTQTSV 297
DB 261 YAGQRYSFILADQYDYNWIRANPGIGITGFGAGGINSAILRYOGADVPEPTTQATSP 320
QY 298 IPLIETNLHPLARMVPVPGSPGVDKALNLAFAFNNGTN--FFTINNATFTPTVPVLLQI 355
DB 321 VVLSSENLAPLTNAAPGLPEVGGVDLALNLTDFDGLSLKFGINGVTFVPPVPLVLLQI 380
QY 356 LSGAQTADLLPAGSVYPLPAHSTTEITLPATAPGAPHPHFLHCHAFVAVRSAGSTTY 415
DB 381 LSGAQAADLLPAGSVYALPSNATLSPALGAL--GGPHFPHLHGHTFSVVRPAGSTTY 438
QY 416 NYNDPIFRDVTSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDPHLDAGFAI 465
DB 439 NYVNPVQRDVVSIGN--TGDNVNTRFDNNPGPWFHLCHIDHLEAALPL 486

RESULT 4

US-09-732-350-1
Sequence 1, Application US/09732350
Patent No. US20010031490A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,350
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-1

Query Match 57.4%; Score 1533; DB 10; Length 539;
Best Local Similarity 59.1%; Pred. No. 2.5e-120;
Matches 295; Conservative 53; Mismatches 137; Indels 14; Gaps 6;

QY 2 IGPVASLVANAPVSPGFLRDAIVNGVVPSPITKGGDRFQNLNVVDLTNHSMLKST 61
DB 21 VNSVDTWLTNANVSPDGFTRAGILVNG-VHCPLLRGKNDNFELNVVNDLNPMLRPT 79
QY 62 SIHHGFFOAGTNWADGPAFVNQCPIASGHSFLYDFHVDPQAGTFWYHSHLSYQCDGL 121
DB 80 SIHHGFFOAGTNWADGPAFVNQCPIASGHSFLYDFHVDPQAGTFWYHSHLSYQCDGL 139
QY 122 GPFVVYDPKPHASRYDVNDSVTITLTDWYHTAARLGPRLGADATLNLGLGRSAS 179
DB 140 GPMVIYDNDPHALYDEDDNTIITLADWYHIPA---PSIOGAAQPDATLINGRKYVG 196
QY 180 TPTAALAVINVQHKRYRFRVLSISCDPNYTFSDGHNLTVEVDGINSQPLLVDSIQI 239
DB 197 GPAEELSIVNVQGGKRYRFRVLSISCDPNYTFSDGHNLTVEVDGINSQPLLVDSIQI 256
QY 240 AAQRYSFVLNANQVGNVWRANPNFGTVG---FAGGINSAILRYOGAPVAEPTTTQTT 295
DB 257 TQORYSFVLNANQVGNVWRANPNFGTVG---FAGGINSAILRYOGAPVAEPTTTQTT 316
QY 296 SVIPLIETNLHPLARMVPVPGSPGVDKALNLAFAFNNGTN--FFTINNATFTPTVPVLLQI 355
DB 317 NPAQNEADLHALIDPAAPGIPITPGAADVNLRFGSGGRFTINGTAYESVPTLLOI 376
QY 356 LSGAQTADLLPAGSVYPLPAHSTTEITLPATAPGAPHPHFLHCHAFVAVRSAGSTTY 415
DB 377 MSGAQSANDLLPAGSVYELPRNQVVELVVPAGVL--GGPHFPHLHCHAFSVVRSAGSTTY 434
QY 416 NYNDPIFRDVTSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDPHLDAGFAI 475
DB 435 NFVNPVKEDVYSLG--VTGDEVNTRFQTDNPGPWFHLCHIDPHLDAGFAI 492
QY 476 AANPVPKAWSDLCPIYDGL 494
DB 493 DANNPVEWAQCEIYDDL 511


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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-732-350-8

Query Match 33.1%; Score 884.5; DB 10; Length 575;
Best Local Similarity 37.5%; Pred. No. 3.7e-66;
Matches 211; Conservative 79; Mismatches 184; Indels 89; Gaps 19;

QY 8 LVANAPVSPDGLRDAIVGVVPSPLITGKGRFQNLNVDTLTNHSMLKSTSIHHWG 67
Db 26 LKISDGEIADPGVKNRATLVGGYPCGLIFANKGTLKVKVQKLTNPENYRTTSIHHG 85
QY 68 FFOAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPFVY 127
Db 86 LLQHRNADDGSPFVTCPIVPRESYTYTIPDDGTGYWYHSHLSQYVDGLRGLVIY 145
QY 128 DPDPHASRYDVDNESVTITLTDWYHTAA-----LGRFPLGADATLNLGLRSAST 180
Db 146 -PKDPHRLYDVDDKTVLIGDWHYESSKAILASGNITRQRPVSA---TINGKGRDPD 201
QY 181 PTAA----LAVINVQHGKRYRFLVLSVSCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSI 236
Db 202 NTPANPDTLTLKVRGKRYRLRVINSEISAFSFEVGHKVTVIAADGVSTKPYQVDAF 261
QY 237 QIFAAQRYSFVLNANQVGNVWRAN---PNFGTVGF-----AGGI 274
Db 262 DILAGRIDCVNEAQEPDIYWINAPLTNPVNTKAQALLVYEDRRPYHPKGPYKWSV 321
QY 275 NSAILRYOG-----APVAEPT-----TTQTSVPILIETNLH 306
Db 322 SEAIKYWNHKKHGRGILLGSHGGLKARMIEGSHLHRSRVKVRQNETTVV-MDESKLV 380
QY 307 PLARMPVPGSTPG-GVDKALNLAFA--NENGTFNFINATFTPTVPVLLQLLSGAQ--T 361
Db 381 PL---EYPGAAGSKPADVLVDLTFLGNFATGHWINGIPIESKIPITLKLITDEGVT 437
QY 362 AQDLLPAGSVYPLPAHSTIETTLPATALAPGAPPHLGHAFVAVRSAGSTTYNYNDPI 421
Db 438 ESDFTKEHTVILPKNKCIEFNKNSGIP-ITHPVHLGHTWDVQ-FGNNPPNYVNP 495
QY 422 PRDVVGTGTPAAGNVITRFOTDNPDPWFHLCHIDFHLADAGFAIVFAEDVADVKAANVP 481
Db 496 RRDVV--GSTDG--VRIQFTDNPDPWFHLCHIDHLEEGFAMVFAEPAVKGG---P 548
QY 482 KA-----WSDLCPIYDGLSEAN 498
Db 549 KSAVDSQWEGLCCKYDNWLSKN 571

RESULT 9
US-09-732-350-9
; Sequence 9, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. US20010031490A1o No. US20010031490A1disk of No. US20010031490A11th
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; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,350
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/032,315
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-732-350-9

Query Match 21.6%; Score 577; DB 10; Length 616;
Best Local Similarity 29.5%; Pred. No. 1.9e-40;
Matches 160; Conservative 82; Mismatches 199; Indels 102; Gaps 21;

QY 10 VANAPVSPDGLRDAI-VVNGVVPSPPLITGKGRFQNLNVDTLTNHSMLKSTSIHHWG 68
Db 89 VDNRP-GPDGVKEKMLINDKLLGPTVFANWGTIEV----TVNNHLRTNGTSIHHGL 143
QY 69 FQAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPFVYD 128
Db 144 HQGTNYHDGANGVTECPPIPGSRVYSFRA-ROYGTSWYHSHFSAQYGVGSGAIQI-- 200
QY 129 PKDPHASRYDVDNESVTITLTDWYHTAA-----RLGPRFPLGADATLNLGLRSASTPT 182
Db 201 -NGPASPYPYDID--LGVLPXLDWYKSAQDLVIETLAKGNAPFSDNYLNGTAKHPPTGE 257
QY 183 AALAVINVQHGKRYRFLVLSVSCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFAAQ 242
Db 258 GEVAIVKLTDPKRRHLRLINNSVENHFQVSLAKHTMTVIAADMVVPVNAVMTVDSLMAVGQ 317
QY 243 RYFVLNANQVGNVWRANPNEG---TVGFA-GGINSAILRYOGAPVAEPT----- 290
Db 318 RYDVTIDASQAVGYWF--NITFGGQOKCGFSHNPAPAAIFRYEGADPALTDPGAAPKD 375
QY 291 --TQTTSTVPIETNLHPLARMPVGS--PTPGGVDKALN---LAFNFGT----- 335
Db 376 HQCLDTLDSLPPVQKNVPVDGFYKPECGNTLPVTLHVDOAAAAPHVFTWKINGSAADVDWR 435
QY 336 ---NFFINNATFTPTVPVLLQLLSGAQTAQDLL---PAGSVYPLPAHSTIETLTPATAL 389
Db 436 PVLEYVMNNDLSSIPVKNVIRVDGVNWTYVWLVEPDEGRL----- 477
QY 390 APGAPHFHLLGHAFV-----VRSAGSTYNY-----NDPIRDRVSTGTPA 432
Db 478 --SLPHPMHLGHDFHVLGRSPDVSPDSETRFVDPDAVDLPRLRGHAPVRDVP--TMLPA 533
QY 433 AGDNVITRFOTDNPDPWFHLCHIDFHLADAGFAIVFAEDVADVKA-----ANPVPKA 483
Db 534 RG-WLLAFRTDNFGANLHFCHIXAHXVSGGLSVDFLERPDELRLQLTGESKALERVCRE 592
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; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080.210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Curvularia pallescens
; US-10-080-210-7

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	Query Match.	6.68;	Score	176.5;	DB	12;	Length	627;
	Best Local Similarity	22.5%;	Pred.	No.	5.2e-07;			
	Matches	121;	Conservative	67;	Mismatches	198;	Indels	151;
	Gaps	34;						
QY	12	NAPVSPDGFERDAIVV--NGVVPSPLITGKGGDRFQLNVVDTLNHSMLKSTSHHGFF	69					
Db	105	NOQWIPS--LRPARLVGYDGISPGPTIIVRGTEAVRVRFVNGQDRES-----SIHLHGSP	157					
QY	70	QAG--TNWADGPFAVNOCPIASGHSEFLYDFHPV--DOAGTF-WYHSHLSLSTQCD----	GLR	121				
Db	158	SRAFPDGAEDLINKGQ-----FKDYYPNNQAARFLWYHDHAMHVTAENAYFGQA	208					
QY	122	GPFWVPDKD-----PIA-SRYDVDNESVTITLDWYHTAARL-----GPREPLGADATLI	171					
Db	209	GAYLITDPADAELGPLSGYKYDI-----PLVLSSKFYNSDGTLTQTSVGEDNSLMGDVIHV	264					
QY	172	NGLGRSASTPAAALAVINVOHGKRRLYSISCOPNYTFSIDGHNLT-----VIEUD	224					
Db	265	NG-----QPWFPEFVE--PRXIRULRNAAVSRNFALYFVKQATATATBLPFQVIASD	314					
QY	225	-GINSQPLLVDISOIFAQRYSFVLN-----ANQTGVNYYVRANFPGTVGVGAGGINS---	276					
Db	315	AGLLTHPVQTSIDIVVAARAERYEIVDFAPYAGQIID--LR--NFAK---ANGVGTD	365					
QY	277	----AILRGOGPAVEPTTTQTTSVPLIETNLHPIARMVPVSGPPGGVDKALNAFN	331					
Db	366	YANTDKVMREHFVSQA-----VVDNSVYPA-----QLSQIOFPADKT--GIDH---	409					
QY	332	FNGTN--FFINNAFTPTVPVLQILSGAQTAODLLPAGSVYPLPAHSTIEITLPATAL	389					
Db	410	FHRNTSWRRINGICFADVQNRIAKV-----PRGIVEIWELENS-----	448					
QY	390	APGAPHFPHLGHAFAVRSAGSTYN-----YNDPIFRDVVYSTCTPAAGDNVITRFOT--	443					
Db	449	SGGWSPITHVLVDFRVARYRGDESTRGMPYESAGLKDVVWLG-----RHETVL	498					
QY	444	--DNPGPW----FLRCHIDFHLDAGFAIVFAEDVADVK-----AANDVPKAMS	485					
Db	499	VEAHYADPDGYMPCFHNLIHEDODMMAAF--DVTKLQFCFYNETTDFDHDPDSRW	553					

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RESULT 15
US-09-338-723A-4
; Sequence 4, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzym
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 627
;

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; TYPE: PRT
; ORGANISM: Bipolaris spicifera
US-09-338-723A-4

[illegible]

Search completed: December 14, 2002, 08:30:34
Job time : 24 sec

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:14:26 ; Search time 66 Seconds

(without alignments)

8987.750 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgccggtgagcag.....tgagcaggtaaccagtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.6	3.8	1965	10	US-09-826-660-26
2	54.6	3.6	88421	9	US-09-976-059-1
3	53.2	3.5	88421	9	US-09-976-059-1
4	50.2	3.3	1722	9	US-09-938-842A-1675
5	47.4	3.2	1488	10	US-09-764-870-209
6	47.4	3.2	2531	10	US-09-764-870-49
7	47.2	3.1	1713	9	US-09-938-842A-1910
8	46.8	3.1	5036	10	US-09-918-951-2
9	46.2	3.1	2010	12	US-10-032-717-9
10	46.2	3.1	2838	10	US-09-954-456-700
11	46.2	3.1	2838	10	US-09-954-456-966
12	46.2	3.1	2838	10	US-09-954-456-1143
13	44.8	3.0	1395	10	US-09-815-242-4093
14	44.2	2.9	2155	10	US-09-962-436-299
15	44.2	2.9	2155	10	US-09-880-107-2394
16	44.2	2.9	6200	9	US-09-993-241-1
17	44.2	2.9	6200	10	US-09-993-038-1
18	43.6	2.9	2163	10	US-09-939-408A-29
19	43.2	2.9	1248	9	US-09-860-846-7

20	43.2	2.9	1248	10	US-09-861-289-7	Sequence 7, Appli
C 21	43.2	2.9	13613	9	US-09-860-846-3	Sequence 3, Appli
C 22	43.2	2.9	13613	10	US-09-861-289-3	Sequence 3, Appli
23	42.8	2.9	2430	9	US-09-860-846-23	Sequence 23, Appli
24	42.8	2.9	2430	10	US-09-861-289-23	Sequence 23, Appli
25	42.8	2.9	4689	9	US-09-860-846-34	Sequence 34, Appli
26	42.8	2.9	4689	10	US-09-861-289-34	Sequence 34, Appli
27	42.8	2.9	13613	9	US-09-860-846-3	Sequence 3, Appli
28	42.8	2.9	13613	10	US-09-861-289-3	Sequence 3, Appli
29	42.8	2.9	36778	9	US-09-860-846-5	Sequence 5, Appli
30	42.8	2.9	36778	10	US-09-861-289-5	Sequence 5, Appli
31	42.4	2.8	2322	10	US-09-476-242-18	Sequence 18, Appli
32	42.4	2.8	2322	10	US-09-476-242-19	Sequence 19, Appli
33	42.4	2.8	2322	10	US-09-476-242-20	Sequence 20, Appli
34	42.4	2.8	2334	10	US-09-476-242-7	Sequence 7, Appli
35	42.2	2.8	1140	9	US-09-860-846-15	Sequence 15, Appli
36	42.2	2.8	1140	10	US-09-861-289-15	Sequence 15, Appli
37	42.2	2.8	1296	10	US-09-815-242-4090	Sequence 4090, Ap
38	42.2	2.8	2712	10	US-09-748-033-4	Sequence 4, Appli
39	42	2.8	1375	10	US-09-770-621-1	Sequence 1, Appli
40	41.4	2.8	491	10	US-09-833-790-353	Sequence 353, App
41	41.4	2.8	1107	10	US-09-748-033-6	Sequence 6, Appli
42	41.2	2.7	424	10	US-09-960-352-12392	Sequence 12392, A
43	41.2	2.7	788	9	US-10-076-785-55	Sequence 55, Appli
44	41.2	2.7	2310	10	US-09-476-242-3	Sequence 3, Appli
45	41	2.7	3189	10	US-09-815-242-4056	Sequence 4056, Ap

ALIGNMENTS

RESULT 1

US-09-826-660-26
; Sequence 26, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-26

Query Match	3.8%;	Score	56.6;	DB	10;	Length	1965;
Best Local Similarity	44.1%;	Pred. No.	66-05;				
Matches	331;	Conservative	0;	Mismatches	414;	Indels	6;
Gaps	2;						
QY	669	CGACGGTATCAACAGCAGCAGCTCTCCTTGTGACTATATCCAGATCTTCCGCCGCGAGCG	728				
Db	1185	CGCGCAGCATCACCTCCACACCCGCTCTTCAACACCAACCGCGCCGCGCATCGA	1244				
QY	729	CTACTCCTTGTGTTGAATGCGAACCAACGGTCGGGAACCTACTGGTCCGCGCAACCC	788				
Db	1245	CTCAGGGCGCGCAATTTCCGGCAACCTCTACGCCAACCCTACGGGTGTCTCTCTCAA	1304				
QY	789	GRACCTCGGACGGTGGTTCGCCCGGGGGATCACTCGCCATCTCTGGCTACCAAGG	848				


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; NAME/KEY: misc_feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

Query Match      3.6%; Score 54.6; DB 9; Length 88421;
Best Local Similarity 46.6%; Pred. No. 0.00049;
Matches 174; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1116 CCGCTCCCGCCGCTCCACCATCGAGATCAGCTGCCGCGACCGCTTGGCCCCGGG 1175
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Db 47206 CCGCGTTCCGGCAAGTTCCAGCTCGACCTCAGCTTACCGAGACCTTCGACGCGCGGG 47265

QY 1176 TGCACCGCACCCCTTCCACCTCAGCGTTCACGCTTCGCGGTCGTTCCGAGCGCGGGAG 1235
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Db 47266 GGAGCGCGCGCGCTCGCGTTCGACCTCATCGGGGCGCGACCTTTCGACGCGGGCAC 47325

QY 1236 CACCGAGTATACTAACAGCCCGATCTCCGCGACGCTGTGAGCAGCGCACGCCCGC 1295
      ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 47326 GGC CGCGCGCGCTCGCGGTACCTGAGCGCGTCTTCGCGCTGCTCGCGCGATCCGCG 47385

QY 1296 CCGCGCGCAACGTCACGATCGCTTCCAGACGACACCCCGCGCGCTGCTCTCTCA 1355
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47386 GCGCGCTCGCGAGGTGACCGCTGAGCGGAGGAGACCGCTCATGCTCGCCGC 47445

QY 1356 CTGCCACATGACTTCCACCTTCGACCGGGCTTCGCGATCGTGTTCGAGAGGACGTTGC 1415
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Db 47446 CGGTGAGGAGCGCGCGCGCTGCCCGATCACCCTGCGCGGCTGCTCGCGGACGA 47505

QY 1416 GGACGTGAGGCGCGCAACCCGTTCCGAGCGGTGTCGACCTGTCGCCGATCTACGA 1475
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 47506 GTGCGCGCGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 47565

QY 1476 CCGGCTGAGCGAG 1488
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Db 47566 CGAGCTGAGAG 47578

RESULT 3
US-09-976-059-1/c
; Sequence 1, Application US/0976059
; Patent No. US20020164747A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
; FILE REFERENCE: 3019-PCT
; CURRENT APPLICATION NUMBER: US/09/976,059
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (3118)..(4032)
; OTHER INFORMATION: ORF 2; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (6665)..(5814)
; OTHER INFORMATION: ORF 4; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (7703)..(6693)
; OTHER INFORMATION: ORF 5; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (9464)..(8130)
; OTHER INFORMATION: ORF 6; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (9691)..(10761)
; OTHER INFORMATION: ORF 7; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (12751)..(10829)
; OTHER INFORMATION: ORF 8; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (13617)..(12802)
; OTHER INFORMATION: ORF 9; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (15203)..(13614)
; OTHER INFORMATION: ORF 10; negative strandedness
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; LOCATION: (15591)..(15863)
; OTHER INFORMATION: ORF 11; positive strandedness
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; LOCATION: (15880)..(19035)
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; OTHER INFORMATION: ORF 13; positive strandedness
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; LOCATION: (39713)..(65800)
; OTHER INFORMATION: ORF 14; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (65826)..(66530)
; OTHER INFORMATION: ORF 15; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (66546)..(67370)
; OTHER INFORMATION: ORF 16; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (67384)..(70059)
; OTHER INFORMATION: ORF 17; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (70059)..(70662)
; OTHER INFORMATION: ORF 18; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (70659)..(71906)
; OTHER INFORMATION: ORF 19; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (73439)..(71964)
; OTHER INFORMATION: ORF 20; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (74216)..(73563)
; OTHER INFORMATION: ORF 21; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (75424)..(74213)
; OTHER INFORMATION: ORF 22; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (75535)..(76464)
; OTHER INFORMATION: ORF 23; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (78110)..(76449)
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; OTHER INFORMATION: ORF 24; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

Query Match 3.5%; Score 53.2; DB 9; Length 88421;
Best Local Similarity 54.0%; Pred. No. 0.0011;
Matches 109; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Qy 1281 CACGGGACAGCCCGCGGCGGACACGTCACGATCCGCTTCAGACGGGACACACCCCGG 1340
Db 74244 CCCTGCCCAACCCAGGAGGACGATGACGATCCGCTGCTGATCGCCGACGATCA 74185
Qy 1341 GCCGTGGTTCTCCACATCGCACTTCACCTCGACCGGGCTTCGGGATCGTGT 1400
Db 74184 GCGATATCGGAGTGGCTGCGCTGATCTCGAGGAGCGCCGACATCGAGGTGT 74125
Qy 1401 GCGAGAGACGTTGGGACGTGAGGCGGGAACCCGTTCCGAGGCGGTGGTGGACCT 1450
Db 74124 GCGGAGGCGGTCGACGCGGTGGCGGGTGGCAGCGCGCAAGCTGCGCGCGGAGCT 74065
Qy 1461 GTGCCGATCTACGACGGGTG 1482
Db 74064 GTGCTGTGGACATCCGCATG 74043

RESULT 4
US-09-938-842A-1675
; Sequence 1675, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1675

; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1675
Query Match 3.3%; Score 50.2; DB 9; Length 1722;
Best Local Similarity 52.5%; Pred. No. 0.0021;
Matches 134; Conservative 0; Mismatches 118; Indels 3; Gaps 1;
Qy 138 CACGTCGTGACACCTTGACCAACACACAGCATCTCAAGTCCACTAGTATCCACTGGCA 197
Db 186 CACGTCATTTATCCAGCTGTCACAAACTCTCCACGAAGTGTGTATATCCATTGGCA 245
Qy 198 CGGCTTCTCCAGGACGACCAACTGGGACAGACCCCGCTTCGTCACACCAAGTCC 257
Db 246 CGGCATACGTCAGAAAGGAGCTCCATCGGCTGATGGAGCAGCAGGTGTGACCCAGTGCC 305
Qy 258 TATTGCTTCGGGCAATTCATTTCTGTAGGACTTCATGTGCCACGAGGACGAGACGTT 317
Db 306 TATTAATCCTGGCGAGACTTTTCACTTACAGTTCAATTGT---CGATAAGCGGGGACACA 362
Qy 318 CTGCTACACACAGTCATCTGTCTACGCAATCTGTGACGGGCTGCGAGGACGTTTCGTGCT 377
Db 363 TTTCTACATGGACACTACGGAATGCAAGATCATCGGGACTATACGAATGTTAATAGT 422
Qy 378 GTACGACCCCAAGGA 392
Db 423 AAGATCACCAAAAGA 437
RESULT 5
US-09-764-870-209
; Sequence 209, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1461)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1467)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1473)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1482)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-209
Query Match 3.2%; Score 47.4; DB 10; Length 1488;
Best Local Similarity 50.7%; Pred. No. 0.0099;
Matches 114; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
Qy 1185 CCCCTTCCACTGACGCTGACGCTTCGCGGTTCGTCAGCGGCGGGGAGCACCACGTA 1244
Db 306 CCCCTACACGCTGAACGCTACGCGCTGCGCTGACTCCGTCGGAGAGATCATCCACA 365
Qy 1245 TAACTACAACGACCGCATCTTCCGCGACGTGTGAGCAGCGGCGACGCCCGCGCGGCGA 1304
Db 366 CTACGACAGTGAACAAGATGTTCCCTGCGCTTCCGGGCGCAAGCTGCCCGGATGG 425

Db 649 CACCAGACCCGTCCTCAATACCTAACCAGCACCACCAACCTGAGCGCGACCTCGGCTCAA 590
QY 1062 GATTCGAGCGTGGCAGACCGCACAAGACCTGCTCCTCGAGCTCTGTCTACCCGCT 1121
Db 589 TCACGGCAGTAACACCCAGACGACCTGGCAGCACAAGCCACCTGACCGCGGAACAC 530
QY 1122 CCGCGCCACTCCACATCGAGATCAGCTGCGCCGACCGCTTGGCCCGGGTGCACC 1181
Db 529 CCGTTGACGGCGGAGAGCCAGCCACCTGACCAGGACCCACACCCAGTCGGCTAG 470
QY 1182 GCACCCCTTCACCTGACGCTGACGCTGCGGCTGCTGCGAGCGGGGAGACAC 1241
Db 469 CCAGGCGCCAGCAGATCGGTGCTGATGACGCTTGCACACCCCGCGCGCTCACGG 410
QY 1242 GTATACACTACAGCCCGATCTTCGGGACGCTGCTGAGCAGGCG 1287
Db 409 CGAAGCGGACATTTGGCGAGCTCTCGCAAGCCATCGCGAGCGGC 364

RESULT 9

US-10-032-717-9
; Sequence 9, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry1218-1
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mo1218-1
US-10-032-717-9

Query Match 3.1%; Score 46.2; DB 12; Length 2010;
Best Local Similarity 49.8%; Pred. No. 0.021;
Matches 117; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 1161 CGCCTTGGCCCGGGTGCACCGCACCCCTTCCACCTGACGCTGACGCTTCCGCTGCGT 1220
Db 882 CCCATGTGAGAACCAAGCGCCAGCTACCGCGAGGTGTACACGACCCGCTCGCGCGCT 941
QY 1221 TCGCAGCGGGGAGCACCACGCTATACTACACGACCCGATCTTCGCGAGCTCGTGAG 1280
Db 942 GAACGTGTCTCTCGCTGGCTCTTGGTACGACAAAGGCCCAAGCTTCGGGTGTATCGATC 1001
QY 1281 CACGGGACCGCGCGCGGGGACACAGCTACGATCCGCTTCCAGACGGACAAACCCGG 1340
Db 1002 CTCGCTATCCGCGCGCGCACGCTGTGACTATACATCACGGGCTCACCGTGTACACCCA 1061
QY 1341 CGCGTGTTCCTCACTGCACATCGACTTCCACCTCGAGCGGGGCTTCGCGATC 1395
Db 1062 GTCCCGCTCCATCTCTCCCGCGCTACATCCGCCCATGCGGCGGCCACACGATC 1116

RESULT 10

US-09-954-456-700
; Sequence 700, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-700

Query Match 3.1%; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 962 GCGTCGACAGGCGCTCAACCTCGCGTTAACTTCAACGGCACCACCTCTTTCATCAACA 1021
Db 209 GCGGCGGAGAGACGCGGACCGCGGACTGCTGCTCTGCGCCAGCTGCGGGGCGCGCGG 268
QY 1022 ACGCGACTTTACGCGCGGACCGCTCCCGGTACTCTCTCCAGATTCTGAGCGTGCAGCA 1081
Db 269 CCGAGCCCCCGGCGGAGCGCGGTCCTCCCGGGCGCTGCGCGCGCGCGCGCGGAGC 328
QY 1082 CGGCACAAGACCTGCTCCTCGAGGCTGTGTACCGGTCCTCCGGCCACTCCACCATCG 1141
Db 329 GCGCCATGACGCGCTGCGCGCGGCTTTCCTGCGCGCTGCGCGCGGCGCGGCGCGCG 388
QY 1142 AGATCAGCTGCGCGGACCGCTTGGCCCGGGTGCACCGGTCACCGCTTCCACCTGCAG 1201
Db 389 AGGCGCGCGGCGCGGACTTTCGCGCAACCGGAGGCTGCGCACCGCGCGCGCTCTACA 448
QY 1202 GTCACGCTTCGCGGTCGTTTCGCGAGCGCGGGGAGCACACGTA 1244
Db 449 GTCCACGCGCGCGTGAGCGCGGAGACGAGACCAAGTA 491

RESULT 11

US-09-954-456-966
; Sequence 966, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76

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; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 956
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-966
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Query Match          3.18; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 962 GCGTCGACAGCGCTCAACCTCGCGTTTAACTTCAACGGCAGCAACTTCTTCATCAACA 1021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 GCGGCGGAGAGCGGACCGCGCACTGCTGCTCTGCCCGAGCTGCGGGGGCGCCCGC 268

Qy 1022 ACGGACTTTCACGCGCGCGGACCGTCCCGGTACTCTCCAGATTCTGACGGGTGCGCAGA 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 CCGAGCCCCCGCGCGAGCGCGTCCCGGGCGGCTGCCCGCGCGCTGCCCGCGGAGC 328

Qy 1082 CCGCACAGACCTGCTCCCTCGAGGCTGTCTACCGCGCTCCCGCGCTTCCACCTGCACG 1141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCGCCCATGACAGCGCTGCCCGCGGCTTGCTTGGCGGCTGGCGCGGACACCCCGC 388

Qy 1142 AGATCAGCTCCCGCGCGGACCGCTTGCGCCCGGTTGCGCGGTTGCGCGGCTTCCACCTGCACG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AGGCGCGCGCGCGCGAGCGCTTCCCGCGCGCTGCCCGCGCGCTGCCCGCGGAGC 448

Qy 1202 GTCACGCTTCGCGGTTCGCGAGCGGGGAGCACCACGTA 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GTCCGACGCGCGCGTGGCGCGGAGCAGAGACGACAAGTA 491
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RESULT 12
US-09-954-456-1143
; Sequence 1143, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
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; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1143
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1143

Query Match          3.18; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 962 GCGTCGACAGCGCTCAACCTCGCGTTTAACTTCAACGGCAGCAACTTCTTCATCAACA 1021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 GCGGCGGAGAGCGGACCGCGCACTGCTGCTCTGCCCGAGCTGCGGGGGCGCCCGC 268

Qy 1022 ACGGACTTTCACGCGCGCGGACCGTCCCGGTACTCTCCAGATTCTGACGGGTGCGCAGA 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 CCGAGCCCCCGCGCGAGCGCGTCCCGGGCGGCTGCCCGCGCGCTGCCCGCGGAGC 328

Qy 1082 CCGCACAGACCTGCTCCCTCGAGGCTGTCTACCGCGCTCCCGCGCTTCCACCTGCACG 1141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCGCCCATGACAGCGCTGCCCGCGGCTTGCTTGGCGGCTGGCGCGGACACCCCGC 388

Qy 1142 AGATCAGCTCCCGCGCGGACCGCTTGCGCCCGGTTGCGCGGTTGCGCGGCTTCCACCTGCACG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AGGCGCGCGCGCGAGCGCTTCCCGCGCGCTGCCCGCGCGCTGCCCGCGGAGC 448

Qy 1202 GTCACGCTTCGCGGTTCGCGAGCGGGGAGCACCACGTA 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GTCCGACGCGCGCGTGGCGCGGAGCAGAGACGACAAGTA 491
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RESULT 13
US-09-815-242-4093
; Sequence 4093, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4093
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-4093

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Query Match 3.0%; Score 44.8; DB 10; Length 1395;
Best Local Similarity 42.7%; Pred. No. 0.042;
Matches 229; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

Qy	873	GACCCAGACGAGTGGTGATCCCGCTTATCGAGACGAACATTGACCCCTCGCTCGCAT	932
Db	414	GGCGCAGAAGATCCGGGTGATCACCAGTTCGCGAACACCTCGGCCCTTGGCGCGGGCT	473
Qy	933	GCCTGTGCCTGGCAGCCGCGACACCCGGGGGGGTGCACAAGCGCTCAACCTCGCGTTTAA	992
Db	474	CTCCACCCGCTGCAACCGAAACCCGACGACGACCCGCGGAATCGCCGGAGCAT	533
Qy	993	CTTCAAGGGACCAACTTCTTATCAACAACGCGACTTTCAGCGCGGACCGTCCCGGT	1052
Db	534	CCTCGACGGCTGCTCTTTCGGCAATGGGACGCGATGTCGGGATCAATCCTGCGACCGA	593
Qy	1053	ACTCTCCAGATTCTCAGCGGTGGCAGACGCCACAAGACTGCTCCTGCAAGCTCTGT	1112
Db	594	CAGATGGCCTCGATCTGGCGCCCTGCTGGAGATGTCAGCGGATCATCCAGCGCTACGA	653
Qy	1113	CTACCGCTCCCGGCCCATCTCAACATCGAGATCAGCTGCCCGGACGCGCTTGGCCCC	1172
Db	654	GATTCTTACCCAGCGCTGGTGTGTACCCACGTCACACAGCTCCATCGAGGGGATCAACCG	713
Qy	1173	GGGTGACGCGACCCCTTCCACTCGACGGTCACGCTTCGCGTTCGTCACGCGCGG	1232
Db	714	CGGGTCCGCTGGACCTGGTGTTCAGTCGATCCCGGACCGGACCGGGCCATGCGAG	773
Qy	1233	GAGCACCAAGTATAACTACAACGACCCGATCTTCGCGACGTCGTGAGCACGGGACGCC	1292
Db	774	CTTCGGCATCAGCCTCAAGATCTCTCAGGAAGGCTTACGAGCGCGGGCTACGCCAAGAGCG	833
Qy	1293	CGCGGGGGGCAACGTCACGTCACGTCGTCAGACGACGAACCCCGGCGCTGTTCCT	1352
Db	834	CGGACCCCTAGGCACAACCTGATGTACTTCAGAGACGGCCAGGGCAGCGGCTCTCGGC	893
Qy	1353	CCACTGCCACATCGACTTCCACTCGACGCGGGCTTCGCGATCGTGTTCGAGAGG	1408
Db	894	CAACGCCACCTACGGCGTTCGACCAAGCAGACACTTCGAGACCCGCGCTATCGGTGG	949

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RESULT 14
US-09-962-436-299
: Sequence 299, Application US/09962436
: Patent No. US20020081301A1
: GENERAL INFORMATION:
: APPLICANT: Soppet, Daniel
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-75
: CURRENT APPLICATION NUMBER: US/09/962,436
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US/60/235,082
: PRIOR FILING DATE: 2000-09-25
: PRIOR APPLICATION NUMBER: US/60/234,924
: PRIOR FILING DATE: 2000-09-25
: NUMBER OF SEQ ID NOS: 568
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 299
: LENGTH: 2155

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-299

Query Match      2.9%; Score 44.2; DB 10; Length 2155;
Best Local Similarity 44.1%; Pred. No. 0.066;
Matches 184; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

Qy 816 GGGGATCAACTCCGCCATCTCGCTACCAAGGCGCACCACTCGCCGAGCCCACTACGAC 875
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1126 GAGCAAGGACAATGCCCTTCCTGAGCTACCAACCCGACACCCCTTCGCGGACGCGAC 1185
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 876 CCAGACGACGTCGGTGATCCCGCTTATCGAGACAACTTGACACCCCTCGCTCGCATGCC 935
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1186 CGCGGGCTTCAGGTCAACAAACACCCGCCGCCAGCTGCAGCTGTGGCGAAGCCGGT 1245
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 936 TGTGCTTGGGAGCCGACACCCGGGGGGGTGCAAGAGCGCTCAACCTCGGTTTAACTT 995
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1246 GCTCAGCGCCATGGGGTGTCTGGCGCTGCTGGATGAGAGGAGAGCTCTGGGCCGAA 1305
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 996 CAACGGCACCAACTTCTTCATCAACACGCGACTTTTCACGCGCCGACCGCTCCCGGTA 1055
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1306 GCAGCGCCGGACCGTCTCTGGACAGCAACACACGCTGGCGGTCTGGCCAGCGCCAC 1365
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1056 CTTCCAGATTCGAGCGGTGGCGAGACGGACACAGACTGTCTCCTGGAGGCTGTGCTA 1115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1366 CCCCAGAGGCGCGCGACGCGTGGCGCGCGCGCGTGTGATCTACGCGACGCGACGAC 1425
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1116 CCGCTCCCGGCCACTCCACCATTCAGATCACGCTGGCCCGCGACCGCTTGGCCCGGG 1175
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1426 CCGGCCACCCCAACCGCACGCTCGCGGTGACCTCGGGCTGGCGGGGTGCCCCCGG 1485
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1176 TGCACCGCACCCCTTCCACCTGCAGGCTACGCGCTTCGCGGTCTGCGACGCGGG 1232
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1486 CCGGGCGTGGCTACGTCACGCGCTACTCGGACAAAGGGCTCTGCAGCCCGGACG 1542
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15
US-09-880-107-2394
; Sequence 2394, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2394
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M74715
US-09-880-107-2394

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[illegible]

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QY	936	TGTTGCTTGGCAGCCCGACACCCGGGGGCGTCGACAAGGGCTCAACCTCGCGCTTTAACTT	995
Db	1246	GCTCAGGCCCATGGGGCTGCTGGCGCTGCTGGATGAGGAGCAGCTCTGGGGCGAAAGTGTCTC	1305
QY	996	CAACGGCACCAACTTCTTCATCAACAAGCGGACTTTACGCGCGCGACCGTCCCGGTACT	1055
Db	1306	GCAGCGCGGGACCGTCTCTGGACAGCAACACACGCTGGGCGTCTTGGCAGGCGCCACGG	1365
QY	1056	CCTCAGATTCTGACGGTGGCGCAGACCGCACAAAGACCTGCTCCCTGCAGGCTCTGTCTA	1115
Db	1366	CCCCCAGGGCCCGGCGGACGCTTGGCGCGCGGCTGTGATCTACGCGAGCGACGACAC	1425
QY	1116	CCCGCTCCCGGCCCACTCCACCATCGAGATCAGCTGCCCGGACCGCTTGGCCCCCGG	1175
Db	1426	CCGCGCCCAACCCAGCGGTGCGGTGACCTTGGGGGTGCGGGGTGCCCGCCGG	1485
QY	1176	TGCACCGCACCCCTTCCACCTGCACGGTCACGCCCTTCGCGGTCTGTCGACGCGCGG	1232
Db	1486	CCCGGGCTGTGTACGTACGCGGCTACCTGGACAAACGGGCTCTGCAGCCCCGACGG	1542

Search completed: December 14, 2002, 06:53:26
Job time : 332 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:07:26 ; Search time 262 seconds
(without alignments)
12893.120 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgccggtggcgag.....tgagcgaggtaccacgtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1500	100.0	1500	21	Trametes versicolor
2	1500	100.0	1500	24	Trametes versicolor
3	917.8	61.2	1563	24	Trametes versicolor
4	892.2	59.5	1497	11	Phenol oxidase (PO)
5	892.2	59.5	1497	11	Sequence encoding
6	890.6	59.4	1497	11	Sequence encoding
7	874.8	58.3	1572	20	T. versicolor lacc
8	871.6	58.1	1572	20	T. versicolor lacc
9	771.3	51.5	2880	17	Laccase-LCC2 gene.

10	755.4	50.4	7986	20	AAZ23937	T. versicolor lacc
11	519	34.6	1722	21	AAA57402	cDNA sequence enco
12	519	34.6	1722	21	AAA57439	cDNA sequence enco
13	515.4	34.4	1822	19	AAV28293	Schizophyllum comm
14	509.4	34.0	1801	24	ABK50850	DNA encoding Lenti
15	472.6	31.5	1170	18	AAK67137	Coprinus cinereus
16	452.8	30.2	2418	17	AAK15598	Laccase-LCC1 gene.
17	448.4	29.9	5762	20	AAZ23938	T. versicolor lacc
18	439.6	29.3	1161	18	AAK67138	Coprinus cinereus
19	413.8	27.6	1874	24	ABK50851	DNA encoding Lenti
20	393.6	26.2	2289	24	ABK50852	DNA encoding Lenti
21	377.6	25.2	1176	18	AAK67136	Coprinus cinereus
22	342	22.8	1835	24	ABK50853	DNA encoding Lenti
23	310.6	20.7	2049	11	AAQ03366	Phenol oxidase (PO)
24	310.6	20.7	2049	11	AAQ03573	Phenol oxidase gen
25	257.8	17.2	3284	20	AAK02677	T. versicolor lacc
26	245.6	16.4	1588	21	AAZ24235	R. solani laccase
27	245.6	16.4	1672	16	AAQ86526	Laccase gene RSLac
28	244	16.3	1588	18	AAK63317	Rhizoctonia solani
29	223	14.9	3566	18	AAK69938	Coprinus cinereus
30	212.4	14.2	2940	18	AAK69937	Coprinus cinereus
31	209.8	14.0	2122	13	AAQ20956	Laccase gene. Phl
32	186	12.4	3327	18	AAK69936	Coprinus cinereus
33	182.8	12.2	2860	17	AAK15601	Laccase-LCC4 gene.
34	156.2	10.4	2925	17	AAK15602	Laccase-LCC5 gene.
35	123	8.2	3116	24	ABK15406	DNA encoding Melan
36	112.6	7.5	2249	18	AAK74283	Cellulose binding
37	112.6	7.5	2279	18	AAK74281	Cellulose binding
38	112.6	7.5	2300	18	AAK74282	Cellulose binding
39	109.4	7.3	2476	18	AAK67234	Scytaldium thermo
40	106.6	7.1	3102	17	AAK15600	Laccase-LCC3 gene.
41	106.2	7.1	3192	18	AAK63318	Myceliophthora the
42	105.2	7.0	3187	17	AAK10922	Laccase gene. Myc
43	105.2	7.0	3192	18	AAK72106	Myceliophthora the
44	105.2	7.0	3192	21	AAZ24236	M. thermophila lac
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ALIGNMENTS

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RESULT 1
AAA09191
ID AAA09191 standard; DNA; 1500 BP.
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AC AAA09191;
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DT 10-AUG-2000 (first entry)
XX
DE Trametes versicolor laccase coding sequence.
XX
KW Laccase; transgenic plant; large scale production; paper; pulp;
KW lignin; degradation; biosynthesis; ds.
XX
OS Trametes versicolor.
XX
PN WO200020615-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23256.
XX
PR 05-OCT-1998; 98US-0103031.
XX
(PROD-) PRODIGENE INC.
XX
Hood E, Howard J, Jilka J;
XX
WPI; 2000-30793/26.
XX
P-PSDB; AAY92248.
XX
Industrial scale laccase production in recombinant corn and maize
PT plants to produce enzymes for use in the paper industry

```

XX PS Claim 9; Page 17-19; 34pp; English.

XX CC The Trametes versicolor laccase gene can be used to create transgenic

CC plants which produce laccase at levels of about 0.01% or higher of the

CC total soluble protein of the plant. The transgenic plants may be used

CC for the large scale production of laccase enzymes. Laccase is mainly

CC used in the paper and pulp industry for breaking down lignin.

CC Conversely, laccase is also involved in lignin biosynthesis and the

CC formation of lignin polymers. It is therefore useful as a biological

CC adhesive for gluing wood (e.g. in the production of plywood, oriented

CC strand board, particle board and medium density fiberboard). Laccase

CC may also be used for catalyzing the oxidation of compounds such as

CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is

CC also used as a marker enzyme in enzyme immunoassays, for the oxidation

CC of steroids and the synthesis of vinblastine (a cytostatic compound

CC used in treating malignant diseases).

XX SQ Sequence 1500 BP; 275 A; 551 C; 402 G; 272 T; 0 other;

Query Match 100.0%; Score 1500; DB 21; Length 1500;

Best Local Similarity 100.0%; Pred. No. 3.2e-284;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGGCGGTCGAGCGCTCGTCTCGGAACGCCGCCGCTCGCGGACGGCTTC 60

DB 1 GCCATCGGGCGGTCGAGCGCTCGTCTCGGAACGCCGCCGCTCGCGGACGGCTTC 60

QY 61 CTTTCGGGATGTCATCGTGGTCAACGGCGTGGTCCCTTCCCGGCTCATCCGGGAAGAAG 120

DB 61 CTTTCGGGATGTCATCGTGGTCAACGGCGTGGTCCCTTCCCGGCTCATCCGGGAAGAAG 120

QY 121 GGAGACCGGTCACAGCTCAAGTGTGTCACACCTTGACCAACACACAGCATGCTCAAGTCC 180

DB 121 GGAGACCGGTCACAGCTCAAGTGTGTCACACCTTGACCAACACACAGCATGCTCAAGTCC 180

QY 181 ACTAGTATCCACTGCGAGCGCTTCTCCAGGCAGGCACCACTGGGACAGGACCCCGCG 240

DB 181 ACTAGTATCCACTGCGAGCGCTTCTCCAGGCAGGCACCACTGGGACAGGACCCCGCG 240

QY 241 TTCGTCAACACAGTGCCTTATGCTTCCGGGATTCATTTCTGTAGACTTCCATGTGCC 300

DB 241 TTCGTCAACACAGTGCCTTATGCTTCCGGGATTCATTTCTGTAGACTTCCATGTGCC 300

QY 301 GACAGGACGAGAACTCTGTGACACAGTATCTGTACGCAATATCTGTACGGGCTG 360

DB 301 GACAGGACGAGAACTCTGTGACACAGTATCTGTACGCAATATCTGTACGGGCTG 360

QY 361 CGAGGACCGTTCGTGTGTACGACCCCAAGGATCCGACGCGGCGGTACGATTTGAC 420

DB 361 CGAGGACCGTTCGTGTGTACGACCCCAAGGATCCGACGCGGCGGTACGATTTGAC 420

QY 421 AACGAGACCGGTATCATCGTTGACGACTGTGTACGACGCGTCCCGGCTCGGCTGCC 480

DB 421 AACGAGACCGGTATCATCGTTGACGACTGTGTACGACGCGTCCCGGCTCGGCTGCC 480

QY 481 AGGTTCCCACTCGGCGGACGCCCGCTCATCAATGTGTTGGCGGTTCGGCTCCACT 540

DB 481 AGGTTCCCACTCGGCGGACGCCCGCTCATCAATGTGTTGGCGGTTCGGCTCCACT 540

QY 541 CCGACCGCGGCTGCTGTGTATCAACGTCAGCTCCAGCGGAAAGCGTACCGCTTCGCTC 600

DB 541 CCGACCGCGGCTGCTGTGTATCAACGTCAGCTCCAGCGGAAAGCGTACCGCTTCGCTC 600

QY 601 GTTTCGATCTCGTGACCCGACATACAGTTTCAGCATCGAGCGGCACAACTGACCGTC 660

DB 601 GTTTCGATCTCGTGACCCGACATACAGTTTCAGCATCGAGCGGCACAACTGACCGTC 660

QY 661 ATCAGGTCGACGGTATCAACGCCAGCCCTCTCTGTGCTACTCTATCCAGATCTTCGCC 720

DB 661 ATCAGGTCGACGGTATCAACGCCAGCCCTCTCTGTGCTACTCTATCCAGATCTTCGCC 720

QY 721 GCGCAGCGGTACTCTCTTGTGTGAATGCAACCAACGGTCGGCAACTACTGGGTCCGC 780

DB 721 GCGCAGCGGTACTCTCTTGTGTGAATGCAACCAACGGTCGGCAACTACTGGGTCCGC 780

QY 781 GCGAACCCGAACCTTCGGAACGGTTGGTTGCGCGGGGGATCAACTCCGCCATCTCTGCCG 840

DB 781 GCGAACCCGAACCTTCGGAACGGTTGGTTGCGCGGGGGATCAACTCCGCCATCTCTGCCG 840

QY 841 TACCAAGGCGCACCTGTCGCGGAGCCCACTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

DB 841 TACCAAGGCGCACCTGTCGCGGAGCCCACTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

QY 901 ATCGAGACGAACCTTGCAACCCCTCGCTCGCATGCTGTGCTGGCAGCCCGACACCCGGG 960

DB 901 ATCGAGACGAACCTTGCAACCCCTCGCTCGCATGCTGTGCTGGCAGCCCGACACCCGGG 960

QY 961 GCGGTGCACAAAGCGCTCAACCTTCGGGTTTAACTTCAACGGGACCAACTTCTTCAACAAC 1020

DB 961 GCGGTGCACAAAGCGCTCAACCTTCGGGTTTAACTTCAACGGGACCAACTTCTTCAACAAC 1020

QY 1021 AACGCGACTTTCACGCGCGGACCGTCCCGGTACTCTCTCAGATTCTGAGCGGTGGCGAG 1080

DB 1021 AACGCGACTTTCACGCGCGGACCGTCCCGGTACTCTCTCAGATTCTGAGCGGTGGCGAG 1080

QY 1081 ACCGCAACAGACCTTGCTCCCTGCAAGCTGTGTACCCGCTCCCGGCCACTCCACCATC 1140

DB 1081 ACCGCAACAGACCTTGCTCCCTGCAAGCTGTGTGTACCCGCTCCCGGCCACTCCACCATC 1140

QY 1141 GAGATCAGCTGCCCGGACCGCTTGCGCGCGGAGTGCACCGCCCTTCCACCTGCAC 1200

DB 1141 GAGATCAGCTGCCCGGACCGCTTGCGCGCGGAGTGCACCGCCCTTCCACCTGCAC 1200

QY 1201 GGTCAACGCTTCGCGGTCGTTTCGCGAGCGCGGGAGACACAGTATAACTACAAGACCGG 1260

DB 1201 GGTCAACGCTTCGCGGTCGTTTCGCGAGCGCGGGAGACACAGTATAACTACAAGACCGG 1260

QY 1261 ATCTTCGCGAGCTGTGAGACGGGACGCGCGCGCGGCGGACGACGTCACGATCCGC 1320

DB 1261 ATCTTCGCGAGCTGTGAGACGGGACGCGCGCGCGGCGGACGACGTCACGATCCGC 1320

QY 1321 TTCAGACGGACAAACCCCGGCGCTGTCTTCCACCTGCCACATCGACTTCCACCTGCAC 1380

DB 1321 TTCAGACGGACAAACCCCGGCGCTGTCTTCCACCTGCCACATCGACTTCCACCTGCAC 1380

QY 1381 GCGGGCTTCGGGATCGTTCGCGAGAGACGTTCCGAGACGTTCCGAGGCGGCGGACCCGGTT 1440

DB 1381 GCGGGCTTCGGGATCGTTCGCGAGAGACGTTTCGCGAGACGTTTCGAGGCGGCGGACCCGGTT 1440

QY 1441 CCGAAGGCTGTCGAGCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA 1500

DB 1441 CCGAAGGCTGTCGAGCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA 1500

RESULT 2

ABA92910

ID ABA92910 standard; cdna; 1500 BP.

XX ABA92910;

AC ABA92910;

XX 09-APR-2002 (first entry)

XX Trametes versicolor laccase I gene.

XX Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;

XX copper; metal cofactor; gene; plant; ds.

XX Trametes versicolor.

XX OS Location/Qualifiers

XX Key 1..1500

XX CDS /*tag= a

XX FT /product= "laccase I"

XX FT /note= "no start codon given"

RESULT 3
ID ABL60268 standard; cDNA; 1563 BP.
XX ABL60268;
XX 23-AUG-2002 (first entry)
XX Trametes versicolor Laccase III encoding cDNA SEQ ID NO 25.
DE Fungi; Thal; Ctal; copper-dependent secreted protein; laccase;
KW Trametes ATX1 homologue; copper transporting ATPase; gene; ss.
XX Trametes versicolor.
XX
FH Key Location/Qualifiers
FT CDS 1..1563
FT /*tag= a
FT /product= "Laccase III"
XX
PN DE10046932-A1.
XX
PD 16-MAY-2002.
XX
PF 21-SEP-2000; 2000DE-1046932.
XX
PR 21-SEP-2000; 2000DE-1046932.
XX
PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
XX
PI Marbach-Ringhandt K, Pfaller R, Uldschmid A;
XX
DR WPI; 2002-445163/48.
DR P-PSDB; ABB77510.
XX
PT Expression system for increased production of copper-dependent enzymes,
PT particularly laccase, includes the gene for a copper homeostasis
PT protein -
XX
PS Example 9; Page 46-48; 58pp; German.
XX
CC The invention relates to an expression system (A) that provides increased
CC expression of copper-dependent secreted proteins (I) in eukaryotic cells
CC comprises a gene (II) that encodes (I) and at least one cooper
CC homeostasis gene (III). (A) is used to express enzymes, especially
CC laccase, that require copper as co-factor. (III) transports copper to the
CC secretory pathway so its overexpression leads to increased yields of (I).
CC The present sequence is that of the Trametes versicolor Laccase III
CC encoding polynucleotide of the invention.
XX
SQ Sequence 1563 BP; 271 A; 603 G; 384 C; 305 T; 0 other;

Query Match 61.2%; Score 917.8; DB 24; Length 1563;
Best Local Similarity 75.8%; Pred. No. 1.9e-170;
Matches 1135; Conservative 0; Mismatches 362; Indels 0; Gaps 0;

QY 4 ATCGGGCGCGTGGGAGCGCTCGTCGCGGAACGCCCGCTCTCGCCGACGGCTTCCTT 63
DB 67 ATCGGTCTCTGTCGCGACCTTACCATCACCAGGAGCGGTGAGCGGCTTCTTCT 126
QY 64 CGGGATGCCATCGTGGTCAACGGCGTGGTTCCTTCCCGCTCATCCGCGGAAGAAGGA 123
DB 127 CGCCAGGCGGTGTCGTGAACGGCGGACCCCTTCCCTCTCATCACCAGTAACATGGG 186
QY 124 GACCGTTCACGCTAACGCTGTCGACACCTTGACACCAACCAAGATGCTCAAGTCCACT 183
DB 187 GATCGGTTCCAGCTCAATGTCATGACACACCTTCAGGACCAACACATGCTGAAGAGCAC 246
QY 184 AGTATCCACTGCGCGGTTCCTTCAGGCGAGGACCAACTGGGACAGCGGACCCCGGTTC 243
DB 247 AGTATTCAGTGCAGCGTTTCTTCCAGAGGACCAACTGGGCGACCGGTCCCGCTTTC 306

QY 244 GTCAACCAAGTGCCTATTGCTTCGGGATTCATTCTGTAGACTTCCATGTGCCGAC 303
DB 307 ATCAACCAAGTGCCTATTGCTTCGGGATTCATTCTGTAGACTTCCATGTGCCGAC 366
QY 304 CAGGAGCAAGTTCCTGTGTACACAGTCACTCTGTGTACCAATCTGTGTACGGGTGGA 363
DB 367 CAGGCTGGCACCTTCTGTGTACACAGTCACTCTGTGTACCAAGTGTGTGTGTGAGG 426
QY 364 GGACCGTTCGCTGTGTGTACACCGGATCCGACGCGGACGCGGTGTGTGTGTGTGT 423
DB 427 GGTTCATTGCTGT 486
QY 424 GAGACAGCGTTCATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 483
DB 487 GACGACAGCGTTCATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 546
QY 484 TTCACACTCGGGCGGACGCGGATCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 543
DB 547 TTCCTCTCGGGCGGACGCGGATCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606
QY 544 ACCGCGCGCTGT 603
DB 607 ACCGCGGACCTCACGT 666
QY 604 TCGATCTCGTGGACCGGACGCTTACGCTTACGCTGAGCGGACCAATCTGACCGTATC 663
DB 667 TCCCTGT 726
QY 664 GAGTGTGAGGATCAACAGCGGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 723
DB 727 GAGACGACTCGATCAACAGCGGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
QY 724 CAGCGCTACTCTCTGT 783
DB 787 CAGCGTACTCTCTGT 846
QY 784 AACCGCAACTCGGAACGGT 843
DB 847 AACCGGAGCTTCGTTAAGT 906
QY 844 CAAGGCGACCACTCGCGAGCGGCTAGCAGCGGACGCTGTGTGTGTGTGTGTGTGTGT 903
DB 907 GATGGCGCGCTGT 966
QY 904 GAGAGCAACTTCACCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
DB 967 GAGGTCAACTTCACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026
QY 964 GTCGACAGGCGCTCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023
DB 1027 GTTGACCTGGCATCAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1086
QY 1024 GCGACTTCACGCGCGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1083
DB 1087 GCGTCTTCACGCGCGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1146
QY 1084 GCACAGCACTCTCTGT 1143
DB 1147 GCGCAGGACTCTCTGT 1206
QY 1144 ATCAGCTGTGCGGACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203
DB 1207 ATCTCTTCCCGCGGACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1266
QY 1204 CAGCGCTTCGCGGT 1263
DB 1267 CAGCGGTTCGCGGT 1326
QY 1264 TTCGCGGAGCTGT 1323
DB 1327 TTCGCGGAGCTGT 1386
QY 1324 CAGAGGACAAACCGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1383

Db 1387 CGACCCGACAAACCCGCGGTGTTCTTCCACTGCCACATCGACTTCCACCTCGAGGCC 1446
QY 1384 GCGTTCGCGATCGTGTTCGACAGGACGTTGCGGACGTGAAGCGCGGAACCGGTTCCG 1443
Db 1447 GCGTTCGCGCGTGTGTTCGCGGAGGACATCCCGGACGTGCGGCGGAACCCGTCGCC 1506
QY 1444 AAGGCGTGTGCGACCTGTGCGCCGATCTACGACGGGCTGAGCGAGGCTAACCACTGA 1500
Db 1507 CAGGCGTGTGCGACCTGTGCGCGACCTAGACGGCGCTGACCCCGACGACCACTGA 1563

RESULT 4

AAQ03367
ID AAQ03367 standard; DNA; 1497 BP.

AC AAQ03367;

XX 18-AUG-1990 (first entry)

DE Phenol oxidase (PO) gene.

KW Phenol oxidase (PO) gene; enzyme.

XX JP02005877-A.

PD 10-JAN-1990.

XX 16-JUN-1988; 88JP-0149103.

PR 16-JUN-1988; 88JP-0149103.

XX (OJIP) OJI PAPER KK.

XX WPI: 1990-053914/08.

DR P-PSDB; AAR05279.

XX Phenol oxidase gene - used for biological pulping, etc.

PS Page 812-813; Fig 2; 14pp; Japanese.

CC It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.

XX Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 59.5%; Score 892.2; DB 11; Length 1497;
Best Local Similarity 74.7%; Pred. No. 1.9e-165;
Matches 1119; Conservative 0; Mismatches 378; Indels 0; Gaps 0;

QY 1 GCATCGGCGCGGTGGCGAGCCTGTCGCGAGCGCCCGCTCTCGCCCGGACGGGCTTC 60

Db 1 GCATCGGCGCGCGGTGGCGAGCCTGTCGCGAGCGCCCGCTCTCGCCCGGACGGGCTTC 60

QY 61 CTTTCGGGATGCCATCGTGTGTCGAACGCGGTGTCCTTCCCGCTCATCACCGGGGAAG 120

Db 61 GCTGTCAGGCTGTGTTGTCAACAATGTTACCCCGGGACCCCTGTCGCGGGAACAAG 120

QY 121 GGAGACCGCTTCCAGCTCAACGCTGTCGACACCTTGACCAACACAGCATGCTCAAGTCC 180

Db 121 GGTGACCGCTTCCAGCTCAACGCTGTCGACACCTTGACCAACACAGCATGCTCAAGAGC 180

QY 181 ACTAGTATCCACTGGCACCGGCTTCTTCCAGGACGAGCACCACCACTGGGACAGCAGCCCGG 240

Db 181 ACGAGTATCCACTGGCATGGCTTCTTCCAGAGGGGACAACTGGGCTGATGTTCCCGG 240

QY 241 TTCGTCAACCATGCGCCTATTGCTTCGGGCAATTCATTTCTAGACATTCACCTGCGCC 300

Db 241 TTTGTGAACCATGCGCCTATTTCCTTGGGCACTGTTCTCTAGGATTTCCAGGTTTCT 300

QY 301 GACAGGCGAGGAACGTTCTGGTACCACAGTCACTCTGTCTAGGCAATACTGTGACGGGCTG 360
Db 301 GACAGGCGAGGTTACCTTCTGGTACCACAGCCACTTGTCCACTAGTACTGTGACGGGCTG 360
QY 361 CGAGGACCGTTTCGTGCTGTACGACCCCAAGGATCCGACGCCAGCCGCTACGATGTTGAC 420
Db 361 CGGGTCTCTTCTGCTGTACGATCCCAATGACCCGACGCGAGTTGTATGACGCTCGAC 420
QY 421 AACGAGACACGGTCAATCAGTTGACCGACTGTTACACACACCGCTGCCGGGCTCGGTCC 480
Db 421 AATGACGACCGGTGATCAACCTCGCGGATTTGGTACACACTCCCGAAGCTCGGCCCC 480
QY 481 AGGTTCCCTACTCGGCGGACGCCAGCGCTCATCAATGGTCTTGGGCGGTGCGGCTCCACT 540
Db 481 GCGTTCCCTACTGGTGGGATGCTACCTTATCAAGGGGCTCGGGGTTCCCGCAGACCC 540
QY 541 CCGACCGCGCGGCTTTCGTGTATCAAGCTCCAGCAGCGGAAGCGCTACCGCTTCCGTCTC 600
Db 541 ACGGCGGCGGACCTCGCAGTCACTCAACGTCACGAGGCGCAAGCTACCGTTTCCGCTG 600
QY 601 GTTTCGATCTCGTGCAGCCGGAACACTACAGTTTCAGCATCGACGGGCACATCTGACCGTC 660
Db 601 GTCTCCCTGTGTGTCGACCCCAACACACGTTTCAGCATCGATGGTCATGATTTGACGATC 660
QY 661 ATCGAGTTCGAGCGGTATCAACAGCCAGCCCTCTCTTGTGTGACTCTATCCAGATCTTCGCC 720
Db 661 ATCGAGTTCGAGTTCCTCACTCACTCGCAACCTCTGGTGGTGTGACTCCATCCAGATTTCCGCT 720
QY 721 GCGACGCTACTCTCTTGTGTGTAATGGAACCAACGCTCGGCAACTACTTGGTGGTCCG 780
Db 721 GCGACGCTACTCTCTTGTGTGTAATGGAATGCGACAGGATCTCGGTAACTACTTGGATTCG 780
QY 781 GCGAACCCGAACCTTCGGAACGGTTGGTTCGCGGGGGGATCAACTCCGCCATCTTCGCGC 840
Db 781 GCGAACCCGAACCTTCGGAACGGTTCGCGGGGGGATCAACTCCGCCATCTTCGCGC 840
QY 841 TACCAAGCGCACAGTTCGCGGAGCCCACTTACGACCGACGACGCTCGGTGATCCGCGCTT 900
Db 841 TACGACGCGCGGACCCCGGTTGAGCCCAACGACGACTAGCTAGCCGACCAAGCCCTG 900
QY 901 ATCGAGACGAACCTTGACCCCGCTCGCTCGCATGCTGTGCTGGGAGCGGACACCGCGG 960
Db 901 AACGAGGTTCGACTTGACCCCGCTCGCCACCATGGCTGTGCCGGTGTCCCGGCTCGCGCT 960
QY 961 GCGCTCGACAAGCGCTCAACCTTCGCGTTAACTTCAAGCGGACCAACTTCTTCATCAAC 1020
Db 961 GGTGTGACACGCTATCAACATGGCTTCAACTTCAATGGTACCAACTTCTTCATCAAC 1020
QY 1021 AACGGACATTTTCAGCGCGCGGACGCTCGCGGTACTCTCTCAGATTTAGCGGTGGCAG 1080
Db 1021 GCGCGAGCTTTGTGCCCCCAACCGTTCGCGGTCTCTGCTCAGATCATCAGCGCGGCCAG 1080
QY 1081 ACCGCAACAGACTGCTCTCGAGGCTGTCTACCGCTCCCGGCCCACTCCACCATC 1140
Db 1081 AACGCCACGATCTCTCCCGTGTGCGAGGCTACTTCCCTCCGTCGAACGGGATATC 1140
QY 1141 GAGATCACGCTGCCCGGACCGCTTGGCCCGGGTGTGACCGGACACCCCTTCCACCTGAC 1200
Db 1141 GAGATCTGCTTCCCTGCTACGCGGCTGCTCGGGTGTGCGGCTTCCACCTTCCACCTG 1200
QY 1201 GGTACGCTTTCGCGGTGCTTTCGACGCGGGGAGACACGATATCACTACACGACCGG 1260
Db 1201 GGTACGCTTTCGCGGTGCTTTCGAGCGGACCGGCTGACGACCGCTTACAACTACGACACCC 1260
QY 1261 ATCTTCCGCGAGCTGCTGAGCACGGGACCGCGCGCGGGGACAACTGACGATCCG 1320
Db 1261 ATCTTCCGCGAGCTGCTGAGCACGGGACCGCTGCGCGGCTGACAACTGACGATCCG 1320
QY 1321 TTCGACAGCGGACAAACCCCGGCGGTGTTCTTCCACTGCGACATCGACTTTCACCTCGAC 1380
Db 1321 TTCGACAGCGGACAAACCCCGGCGGTGTTCTTCCACTGCGACATCGACTTTCACCTCGAC 1380
QY 1381 GCGGGCTTCGCGATCGTGTTCGACAGGAGCTTTCGCGGACGTTGAAGCGGCGGACCGGTT 1440

[illegible]

RESULT 6	
AAQ03572	
ID	AAQ03572 standard; DNA; 1497 BP.
XX	
XX	AAQ03572;
DT	03-FEB-1991 (first entry)
XX	
DE	Sequence encoding phenol oxidase (PO).
XX	
KW	Paper pulping; ds.
XX	
PN	JF02027986-A.
XX	
PD	30-JAN-1990.
XX	
PF	15-JUL-1988; 88JP-0175236.
XX	
PR	15-JUL-1988; 88JP-0175236.
XX	
PA	(OJIP) OJI PAPER KK.
DR	WPI; 1990-323326/43.
DR	P-PSDB; AAR07089.
XX	
PT	New phenol oxidase gene - has DNA encoding specified sequence of
PT	499 aminoacid(s)
XX	
PS	Claim 5; Fig 3; 15pp; Japanese.
XX	
CC	PO is useful in biological paper pulping and bleaching.
XX	
SQ	Sequence 1497 BP; 272 A; 536 C; 377 G; 312 T; 0 other;
	Query Match 59.4%; Score 890.6; DB 11; Length 1497;
	Best Local Similarity 74.7%; Pred. No. 3.9e-165;
	Matches 1118; Conservative 0; Mismatches 379; Indels 0; Gaps
QY	1 GCCATCGGGCGGTGGGAGCCTCTGTCGCGGAACGCCCCCCTCTCGCGCCGACGGCTTC 60
Db	
	1 GCCATTGGGCCCAACCCTTGACTCACCATCTCCAATGCCGAGTCAAGCCCGATGGGTTC 60
QY	61 CTTCGGGATGCCATCGTGGTCAAACGGCGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG 120
Db	
	61 GCICGTGAGCTGTGGTTGTCAACAATGTTACCCGGGACCCCTCGTCGGGGCACAAAG 120
QY	121 GGAGACCGCTTCAGATCAACGTCGTCGACACCTTGACCAACACACAGCATGCTCAAAGTCC 180
Db	
	121 GGTGACCGCTTCCAACATCAATGCATCGACAACCTCACGAACCCACACTATGCTGAAGAGC 180
QY	181 ACTAGTATCCACTGGACGGCTTCTCCAGGCAAGGCACCACTGGCGCAGCAGGACCCGGC 240
Db	
	181 ACAGTATCCACTGGCATGGCTCTTCTCCAGAGGGGACAACTGGCTGATGGTCCCGCG 240
QY	241 TTGCTCAACAGTGCCCTATTGCTTCGGGCATTCAATTTCTGTACCAGTTCCATGTGCC 300
Db	
	241 TTGTGTAACAGTGCCCTATTCTCTGGCACTCGTTCTCTACGATTTCCAGGTTCT 300
QY	301 GACCAAGCAGGAACGTTCTGGTACCACAGTCATCTCTACGCAATACTGTGACGGGCTG 360
Db	
	301 GACCAAGCCGTAACCTTCTGGTACCACAGCCACTTGTCCACTCAGTACTGTGACGGCCTG 360
QY	361 CGAGGACCGTTCTCGTGTACGACCCCAAGGATCCGACGCCAGCCGCTACGATGTTGAC 420
Db	
	361 CGGGGTCCTTTCTGGTGTACGATCCCAATGAGCCCCGACGCGAGTTGTTGATGACGTCGAC 420
QY	421 AACGAGACACGCTCATCGTTGACCGACTGTGTACCAACACCGCTGCCCGGCTCGGTGCC 480
Db	
	421 AATGACGACCGGTGATCAACCTCGGGATTGTTACCACTGCCGGAAGCTCGGCCCC 480
QY	481 AGGTTCCCACTCGCGCGGACGCCACGCTCAATAAATGGTCTTGGGCGGTTCGGCTCCACT 540
Db	

[illegible]

RESULT 7
AAx02671
ID AAX02671 standard; cDNA to mRNA; 1572 BP.
XX
AC AAX02671;
XX


```

RESULT 8
AA02672
ID AAX02672 standard; cDNA to mRNA; 1572 BP.
XX
AC AAX02672;
XX
DT 10-MAY-1999 (first entry)
XX
XX T. versicolor lacasee TV-1 cDNA from clone plac56.
XX
XX Lacasee; TV-1; delignification; pulp; depolymerisation; waste water;
KW high-molecular-weight aggregates; delinking; waste paper; polymerisation;
KW aromatic compound; lignin; pulp bleaching; oxidising dye; activating dye;
KW pigment formation; organic synthesis; ss.
XX
OS Trametes versicolour.
XX
XX DE19724039-A1.
XX
XX 10-DEC-1998.
XX
XX 06-JUN-1997; 97DE-1024039.
XX
XX 06-JUN-1997; 97DE-1024039.
XX
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX
XX Pfaller R, Wich G;
XX
XX WPI; 1999-036087/04.
XX
XX New DNA encoding Trametes versicolor lacasee protein - used to e.g.
PT delignify pulp, depolymerise high molecular weight aggregates, delink
PT waste paper, polymerise aromatic compounds in waste water, activate
PT dyes and to couple organic compounds
XX
XX Claim 1; Page 15-17; 42pp; German.
XX
XX This invention describes novel lacasee proteins isolated from Trametes
CC versicolor which can be used in methods for delignifying pulp,
CC polymerising high-molecular-weight aggregates, delinking waste paper,
CC polymerising aromatic compounds in waste water (especially
CC lignin-containing waste water from pulp bleaching), oxidising dyes or
CC activating dyes for pigment formation, or in organic synthesis for
CC coupling aromatic compounds or for oxidising aromatic side chains.
XX
XX Sequence 1572 BP; 269 A; 558 C; 429 G; 316 T; 0 other;
XX
XX
XX Query Match 58.1%; Score 871.6; DB 20; Length 1572;
XX Best Local Similarity 74.0%; Pred. No. 2e-161;
XX Matches 1105; Conservative 0; Mismatches 389; Indels 0; Gaps
XX
Qy 4 ATCGGGCCGGTGGCGAGCTCGTGGCGGAACGCCCGCTCGCCGACGGCTTCTT 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 ATCGGGCCGGTGTCTGACCTTACGATCTCAATGGGTGTGTCGCCGATGGCTTCT 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 64 CGGGATGCCATGTGGTGTCAACGGCGTGGTCCCTTCCCGCTCATACCGGGAAGAGGA 123
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 CGCGCGCGGTGCTCGCGAAGAACACAGGCTCCGGGCGCTCTCATCACGGCCAGATGGC 198
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 GACCGGTTCACGCTCAACGCTGTCGACACCTTGACCACACACGATGCTCAAGTCCACT 183
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 GACCGGTTCAGATCAATGTGTCAACAGCTGTGCGAACACACCATGCTTAAATCGACC 258
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 AGTATCCACTGGCAGCGCTTCTTCCAGGCGAGGACCAACTGGGAGACGCCCGCGTTC 243
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 AGCATCCACTGGCAGCGCTTCTTCCAGAGGCGACGACTGGGCGGACGGCCGTTCGCTTC 318
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 244 GTCAACAGTGGCCCTTATTCGTTCCGGGCATTCATTTCTGTACGACTTCCATGTCCCCGAC 303
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 GTCAACCAATGCCCATTCGCGAGGCGCACTGTTCTCTTTACGACTTCCAGTTCGCGGAC 378
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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|||||
Db 1459 GCGTTCCGCGTGCATGCGCTGAAGACATCCCGGACACCAAGCGCGACACCCCTGCTCT 1518
QY 1444 AAGCGGTGTCGGAAGCTGTGCCGCTACGACGGCTGAGCGAGGCTTAACAG 1497
|||||
Db 1519 CAGGCGGTGTCAGACCTTGGCCCAATCAGACGCGCTCGAGCGCTGAGACGAG 1572

RESULT 9
AAAT15599
ID AAAT15599 standard; DNA; 2880 BP.
XX
AC AAAT15599;
XX
DT 07-APR-1996 (first entry)
XX
DE Laccase-LCC2 gene.
XX
KW Laccase-LCC2; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pDSY19;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ss.
XX
OS Polyporus pinsitus.
OS Trametes villosa.
XX
PH Key Location/Qualifiers
FT CDS 364..2492
FT /*tag= a
FT /product= Laccase-LCC2
FT /note= "EC-1.10.3.2"
FT sig_peptide 364..423
FT /*tag= b
FT exon 364..543
FT /*tag= c
FT intron 544..592
FT /*tag= d
FT exon 593..661
FT /*tag= e
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FT exon 1816..1872
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FT intron 1873..1928
FT /*tag= t
FT exon 1929..2135
FT /*tag= u
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intron 2136..2195
exon /*tag= v
2196..2492
/*tag= w
W09600290-A1.
04-JAN-1996.
15-JUN-1995; 95WO-US07536.
15-MAY-1995; 95US-0441147.
24-JUN-1994; 94US-0265534.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
WPI; 1996-068874/07.
P-PSDB; AAR90722.
DNA constructs for expression of Polyporus laccase enzymes - for use
in e.g. lignin manipulation, juice mfr., phenol polymerisation and
phenol resin prodn
Claim 5; Page 62-65; 137pp; English.
The sequence encodes laccase-LCC2 (pI 5.95) from Polyporus pinsitus
(Trametes villosa). Polymerase chain reaction (PCR) amplification of
P. pinsutus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
a 1500 bp fragment, which is joined to a signal peptide sequence
from a 43-kDa cellulase using primer pHD433 (AAT15605) and a pUC
forward primer in PCR. Clones are expressed in Aspergillus oryzae,
and a cDNA probe is obtained and used to screen a P. pinsutus
genomic library in Escherichia coli DH5-alpha, giving plasmid
pDSY19 (23GEN), with a 4-kb HindIII insert (NRRL B-21266).
Screening also results in isolation of LCC1 (AAT15598) and LCC3-LCC5
(AAT15600-T15602), which encode different laccases produced by P.
pinsutus. The laccases may be used to polymerise lignin or
lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
precursors, in hair dye compositions, or to polymerise or oxidise a
phenolic or aniline compound. These new laccases are well-expressed
in Aspergillus spp. (with vector integration in the genome), in
contrast to previous basidiomycete laccases, which give low yields
of recombinant enzyme.
SQ Sequence 2880 BP; 547 A; 908 C; 793 G; 632 T; 0 other;
Query Match 51.5%; Score 771.8; DB 17; Length 2880;
Best Local Similarity 70.7%; Pred. No. 6.6e-142;
Matches 1463; Conservative 0; Mismatches 37; Indels 569; Gaps 10;
QY 1 GCCATCGGCGCGTGGCGAGCGCTGCTGTCGGAACGCCCGCTCCCGGAGCGGCTTC 60
|||||
Db 424 GCCATCGGCGCGTGGCGAGCGCTGCTGTCGGAACGCCCGCTCCCGGAGCGGCTTC 483
QY 61 CTTGCGGATGCCATCGTGGTCAACGGCGGTGCTCCCGCTCATCACCGGGAAGA-- 118
|||||
Db 484 CTTGCGGATGCCATCGTGGTCAACGGCGGTGCTCCCGCTCATCACCGGGAAGAAG 543
QY 119 -----AGGAGAGCCGCTT 131
|||||
Db 544 GTCGGCGTGTTCGTCGTGCTCTACTCCTTTGCTGACAGCGATCTACAGGGAGACCGCTT 603
QY 132 CCAGCTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATC-- 189
|||||
Db 604 CCAGCTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATC 663
QY 190 -----CACTGGCA 197
Db 664 AAGTGTGACGATCCGAATGTGACATCAATCGGGGCTAATTAACCGCGCACAGCACTGSCA 723
|||||
```

Qy	198	CGGCTTCCTCCAGGCAGGCACCAACTGGCGCAGACGGACCCCGCTTGTGTCFAACAGATGCCCC	257
Db	724	CGCGTTCCTTCAGCGAGGCACCAACTGGGCAGGAAGGACCCGCGTTCGTCFAACCACTGCC	783
Qy	258	TATTGTCTCCGGGCATTCATTTCTGTACGACTTCCTCATCTGCCGACCAAGCA	309
Db	784	TATTGTCTCCGGGCATTCATTCCTGTACGACTTCATGTGTCGCCACGACGAGTAAAGCAG	843
Qy	310	-----	GGAA 313
Db	844	GATTTTCTGGGGTCCCGGTGATGCAATGTCTCATCTCCGACGCTGATCGACAGGGGA	903
Qy	314	CGTTCGTGTACCACTCATCTGTCTACGCAATAGTGTACGGGCTGCGAGGACCGTTGCG	373
Db	904	CGTTCGTGTACCACTCATCTGTCTACGCACTGTGTACGGGCTGCGGGGCGCGTTGCG	963
Qy	374	TCGTGTACGACCCCAAGGATCCGACGCGACGCGCTACGATGTTGTGACAAC	423
Db	964	TCGTGTACGACCCCAAGGACCGCGACGCGCTACGATGTTGTGACAATGTACGTGCGC	1023
Qy	424	-----	CAGAGCAGGTCATCAC 440
Db	1024	CACGGAGTATATCACACACATGCGTTGACGTGCGGCCAACAGGAGACGCGTCATCAC	1083
Qy	441	GTTGACCGACTGGTACCACACCGCTGCCCGGCTCCGGTCCCAGGTGCCA	489
Db	1084	GTTGACCGACTGGTACCACACCGCTGCCCGGCTCCGGTCCCAGTTCCCAAGTTCCCAAGTCTCGCA	1143
Qy	490	-----	CTCGGGCGGACGCCA 505
Db	1144	ATGGCTTAGTGTTCACAGGTTCTTGTGTTATGTTGCTTTCGATGATCGGGCGGACGCCA	1203
Qy	506	CGCTCATCAATGTCTTGGCGGCTCGGGCTCCACTCCACACCGCGCGTGTCTGTATCA	565
Db	1204	CGCTCATCAAGGCTCTGGGCGGCTCGGCTCGACTCCACACGCTGCGCTTGGCGTGTATCA	1263
Qy	566	ACGTCCAGCAGCGAAGCGC-----	585
Db	1264	ACGTCCAGCAGCGAAGCGCGTGAACAATCTCTTGTATGCCAATTCATGCTTTGTGCTG	1323
Qy	586	-----	TACCGTTCCTCGTCTCGTTTTCGATCTCGTGCAGACCGCAACTA 626
Db	1324	ACCTATCGGAACCGCGCAGTACCGCTTCCTGTTCTGTTGATCTGTCGACCGCAACTA	1383
Qy	627	CAGCTTCAGCATCGAGCGGCAACAATCTGACGCTCATCGAGTCTGACGGTATCAACAGCCA	686
Db	1384	CAGCTTCAGCATCGAGCGGCAACAATCTGACGCTCATCGAGTCTGACGGCATCAATAGCCA	1443
Qy	687	GCCTCTCTTGTGCTGCTATCCAGATCTTCGCGCGCAGCGCTACTCTCTTGTG-----	740
Db	1444	GCCTCTCTTGTGCTGCTATCCAGATCTTCGCGCGCAGCGCTACTCTCTTGTGTTAAG	1503
Qy	741	-----	GTTGAATCCGA 751
Db	1504	TCCTTGGCTTTCGATGCTCCAAAGTGGCTCACTCATATACTTTCTGTTAGTTGAATCCGA	1563
Qy	752	ACCAAAAGTTCGCAACTACTGGTCCGGCGAACCAGAACTTCGGAACGGTTGGGTTGCG	811
Db	1564	ATCAACAGTGGGCAACTACTGGTTCGTGCGAACCAGAACTTCGGAACGGTTGGGTTGCG	1623
Qy	812	CCGGGGGATCAACTCCGCCATCTCTGGCTACGAAGCGCACAGTCCGCGAGCCCCACTA	871
Db	1624	CCGGGGGATCAACTCCGCCATCTTGGCTACGAGGCGCACCGGTCCGCGAGCGCTACCA	1683
Qy	872	CGACCCAGACGAGTCCGTTGATCCCGTTATCGAGACGAACCTTGCACCCCTCTCGCTCGCA	931
Db	1684	CGACCCAGACGAGTCCGTTGATCCCGCTCATCGAGACGAACCTTGCACCCCTCTCGCGCA	1743
Qy	932	TGCTCTGT-----	938
Db	1744	TGCCAGTGTATGTCTCTTTTTTCTGATCATCTGAGTTGCCCGTTGTCACCGCATTAATGT	1803
Qy	939	-----	GCTTGGCAGCCGACACCGGGGCGCTCGACAAGGCGCTCAACCTCGCG 987

Db	1804	GT	TACTAT	TAGCCT	GGCAGCGC	ACACCGGGGGCGTGC	ACAAGGCGCTCA	CAACCTCGCG	1863
Qy	988	TTT	AACTTC	-----	-----	-----	-----	-----	996
Db	1864	TTT	AACTTC	CGTAAG	TATCTCTACT	TAAGCTGAGGCTCGT	CGCTGATCAT	ACGGTGC	1923
Qy	997	----	----	ACGGC	ACCACTTC	TTCATCA	CAACGCGAC	TTTACGCCGCGACCGTCCCGG	1051
Db	1924	TT	CAGAA	CGGCACTTCT	TTCATCA	CAACGCGAC	TTTACGCCGCGCGACCGTCCCGG	1983	
Qy	1052	TAC	TCCTCC	AGATTCT	GAGCGGTG	CGCAGACGCGCA	AGAAGCTGCTCCCTCGACGGCTCTG	1111	
Db	1984	TAC	TCCTCC	AGATTCT	GAGCGGTG	CGCAGACGCGCA	AGAAGCTGCTCCCGCGAGGCTCTG	2043	
Qy	1112	TC	TACCGCGCT	CCGGCCCACT	CCACCATCG	AGATCACGCTGCCCGCGACCGCGCTTGCGCC	1171		
Db	2044	TCT	ACCGCGCT	CCGGCCCACT	CCACCATCG	AGATCACGCTGCCCGCGACCGCGCTTGCGCC	2103		
Qy	1172	CG	GTGCAC	CGACCCCTTCC	CACTGC	ACGGT-----	-----	1203	
Db	2104	CG	GTGCAC	CGCACCCCTTCC	CACTGC	ACGGT-----	-----	2163	
Qy	1204	-----	-----	-----	-----	-----	-----	1231	
Db	2164	CCG	GAACAG	TGCTCAG	TCGCTCCGTC	CCATCTAG	ACGCGCTTCGCGGTCGTTCCGAGCGGG	2223	
Qy	1232	GG	ACACCA	GTATACT	ACAACGACCCCG	ATCTCCGCGACGTCGTG	AGCAGCGGCGACGC	1291	
Db	2224	GG	ACACCA	GTATACT	ACAACGACCCCG	ATCTCCGCGACGTCGTG	AGCAGCGGCGACGC	2283	
Qy	1292	CCG	CGCGGGG	CGACAGGT	CACATCCGCTTC	ACAGCGACACCCCGCGCGCTGGTTC	1351		
Db	2284	CCG	CGCGGGG	CGACAGGT	CACATCCGCTTC	ACAGCGACACCCCGCGCGCTGGTTC	2343		
Qy	1352	TCC	ACTGCC	ACATCG	ATTCC	ACCTCGACGCGGGGTTCG	CGCATGCTGTTTCG	AGAGGACG	1411
Db	2344	TCC	ACTGCC	ACATCG	ATTCC	ACCTCGACGCGAGGTTTCG	CGCATGCTGTTTCG	AGAGGACG	2403
Qy	1412	TTG	CGGAGTGA	AGGGGGCA	CCCGTTC	CGAAGCGGTG	TCGCGACCTGTG	CCCGATCT	1471
Db	2404	TTG	CGGAGTGA	AGGGGGCA	CCCGTTC	CGAAGCGGTG	TCGCGACCTGTG	CCCGATCT	2463
Qy	1472	AC	GACGGGCT	GACGAGGCT	TAACCA	GTGA	1500		
Db	2464	AC	GACGGGCT	GACGAGGCT	TAACCA	GTGA	2492		

RESULT 10	
AAZ23937	
ID	AAZ23937 standard; DNA; 7986 BP.
XX	
AC	AAZ23937;
XX	
DT	27-JAN-2000 (first entry)
XX	
DE	T. versicolor laccase I DNA.
XX	
KW	Filamentous fungus; hydrolytic enzyme; cellulase; hemicellulase;
KW	lipase; oxidoreductase; lignin peroxidase; mangan peroxidase;
KW	cellobiose-chitin oxidoreductase; cellobiose-oxidase; laccase I; ss.
XX	
OS	Trametes versicolor.
XX	
PN	WO9951757-A1.
XX	
PD	14-OCT-1999.
XX	
PF	01-APR-1999; 99WO-EP02252.
XX	
PR	02-APR-1998; 98DE-1014853.
XX	
PA	(CONE) CONSORTIUM ELEKTROCHEM IND GMBH.


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QY 841 TACCAGGCGCAGCAGTCCCGAGCCCACTACGACCCAGCAGCGTCGGTGATC----- 894
Db 991 TATATCGGCGCTCTCTCCGAGCCGCTGAGTGCATACGAGCCGCTCTCTCTTGG 1050
QY 895 CCGCTTATCGAGCAGCACTTGCACCCCTCGCTCGCATCCCTGTGCTGGCAGCCGACA 954
Db 1051 CTTTGTGGAGACCGCCCTCCGTCTCTCGAGAACCTTGGCGCGCTGGTCTCCGCCAG 1110
QY 955 CCGGGGGCGTCGAAAGCGCTCAACCTCGCGTTTAAAC-----TTCAACGGCACCAAC 1008
Db 1111 CAAGGGGAGCGAGTGAACATCAACCTCGCGATGACCTTACGCTGACCCATTCAG 1170
QY 1009 TTCTTCATCAACAACGCGACTTTCAGCGCGCGAGCCGTCGCTACTCTCCAGATCTTG 1068
Db 1171 TTCAGGGTGAACGGCGCGCATTCATTCGCGGAGTCTCGCGGTGCTGTGAGGTGAG 1230
QY 1069 ACGGTGGCAGACCGCACAAACCTGCTCCCTCGAGGCTGTCTACCCGTCGCGGCC 1128
Db 1231 AGCGGAGCGGTACTGCGCAGGAGTGTTCGGAAGGAGCGGTACACGCTACCGGCC 1290
QY 1129 CACTCCACCATCGAGATCACGCTGCGCGACCGCTTGGCCCGCGGTGCACCGCACCC 1188
Db 1291 AACCAGCGTTGAGATATGATAC-----CCGGCGGAGTGTGGAGCCCTCATCTT 1344
QY 1189 TTCCACCTGCACGGTCAACGCTTCGCGGTTCGCGAGCGCGGGAGCAGCAGTATAC 1248
Db 1345 TTCCATTTGCACGGGACATCGTTCGACGTTGTCGAGCGCGGGAGCAGGACTACAA 1404
QY 1249 TACAAGACCCGATCTTCGCGACGCTGTGAGCAGCGGCGCCGCGCGGGGACAAAC 1308
Db 1405 TACGGAATTCGATTCGCGGAGCGTGTGCAACACGGGCTTG-----GCTGGTACAA 1458
QY 1309 GTACGATTCGCTTCAGACGAGCAACCGCGCGGTGTTCTCTCCACTGCCACATCGAC 1368
Db 1459 ACTAGATTCGATTACGAGACAGCAATTCGCGGCGCTGGATTCATTCGATATGAC 1518
QY 1369 TTCCACCTGCAGCGGGCTTCGCGATCGTGTTCGAGAGGAGTTCGCGACGTGAAGCG 1428
Db 1519 TGGCACCTCGACATCGGTCTCGCGCTGTGTGATGGCAGAGGAC---ACGATGGTATGG 1575
QY 1429 GCGAACCCGGTTCGAGCGGTGTCGACCTGTCCCGATCTACGAGGGGTGAGCGAG 1488
Db 1576 CAGTCCGTACGCCAACTGCATACAGTATCTCTGCCAAGTACGACGCGTGTCTGAC 1635
QY 1489 G 1489
Db 1636 G 1636
```

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RESULT 14
ABK50850
ID ABK50850 standard; DNA; 1801 BP.
XX
AC ABK50850;
XX
XX 30-JUL-2002 (first entry)
XX
XX DNA encoding Lentinula edodes protein with laccase activity #1.
XX
XX Laccase; enzyme; gene; ds.
XX
XX Lentinula edodes.
XX
XX Key Location/Qualifiers
XX CDS 47..1603
XX /*tag= a
XX /product= "Lentinula edodes protein with laccase
XX activity"
```

JP2002065282-A.

05-MAR-2002.

XX

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PF 04-SEP-2000; 2000JP-0267473.
XX
PR 04-SEP-2000; 2000JP-0267473.
XX
PA (IWAT-) IWATE KEN.
XX
XX WPI; 2002-377662/41.
DR P-PSDB; AAU96688.
XX
XX New proteins derived from Lentinula edodes for use in providing laccase
PT enzyme activity -
XX
XX Claim 3; Page 13-15; 30pp; Japanese.
XX
XX The invention describes novel proteins derived from the species
CC Lentinula edodes and having laccase enzyme activity. This sequence
CC encodes a Lentinula edodes protein having laccase activity.
XX
XX Sequence 1801 BP; 419 A; 480 C; 383 G; 519 T; 0 other;
```

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Query Match 34.0%; Score 509.4; DB 24; Length 1801;
Best Local Similarity 61.1%; Pred. No. 1.2e-90;
Matches 917; Conservative 0; Mismatches 566; Indels 18; Gaps 5;
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QY 1 GCATCGGGCGGTGGCGAGCCTCGTCGCGAAGCGCCCGCTCTCGCCCGACGGCTTC 60
Db 101 GCCATCGGTCTGTCACCTGTCATATCGTGAACCTGTTTCACTCAACCTGACGGCTTC 160
QY 61 CTTTCGGGATGCCATCGTGGTCAACGCGGTGCTCCCTTCCCGCTCATCACCGGGGAAG 120
Db 161 AACCGCTCTGGTGTCTTCTGCTGAGGCGCTTCTTCTGGACCACTCATCACGGTAACAAA 220
QY 121 GGAGACCGGTTCCAGCTCAACGCTGTCGACACCTTGACCAACACAGCATGCTCAAGTCC 180
Db 221 GCGCAATTTCCAGATCAATGTGATGATGAGCTCACTAAGCAACGATGCTTTGAGC 280
QY 181 ACTAGTATCCACTGGCAGCGCTTCTTCAGGCGAGGCAACCACTGGGCGACGAGCCCGG 240
Db 281 ACTTCGATTCATTGCGACGGCCCTTTTCAGAAAACAACTGGGCGACGAGCAGCA 340
QY 241 TTCGTCAACAGTGGCTTATGCTTCGCGGCAATTCATTTCTGTAGACATTCATGTGCC 300
Db 341 TTCGTGAATCAATGCTTATCGCGCGAATGATGCTTCTCTGTACAAATTTCAATGTCCG 400
QY 301 GACGAGGAGGAACCTTCTGTACCACTCATCTGTCTACGCAATCTGTGTCACGGCTG 360
Db 401 GACCAAGTGGAGCTTCTGGTATCACAGTCACTATCCACTCAATATTGCGATGATTG 460
QY 361 CGAGGACGCTTCTGTGTACGACCCCAAGGATCCGCGACGCGCGCTACGATGTTGAC 420
Db 461 CGTGACCCCTTGGTGTGTATGACCCCTCAAGATCCATAGCTGACCTATACGAGCTTGAT 520
QY 421 AACGAGACGAGGTATCATCGTTGACCGACTGTTACCAACCGCTGCGCGGCTCGGTGCC 480
Db 521 GATGATTCAACTGTCTACACTCGCTGCTGATGATGATGATGATGATGATGATGATGAT 580
QY 481 AGGTTCCACTCGGCGGCGACCGCTCATCAATGTTGTTGGGCGGTGCGCTCCACT 540
Db 581 GCTGTTCGACCT---CGGACGCGCTCTCATCAATGGCTAGGAGATTCGCTCAACGGT 637
QY 541 CCCACCGCGCGC---TTGCTGTGATCAACGCTCCAGCAGCGGAAAGCGCTACCGCTTCCG 597
Db 638 CCAGCGGATGACCCCTTTGCTGTAGTCAATGCTGAGGAGTGTGCTGATGCTGATGCTG 697
QY 598 CTCGTTTCGATCTCGTGGACCGCACTACAGTTTACAGTTCAGCATCGCGGCGACATCTGACC 657
Db 698 TTGGTGTGATCTTGTGATCCGAACTTCTGTTTTCGATGACGCGGCGACACCTTTACT 757
QY 658 GTCATCGAGGTGCGCGGTATCAACGCGAGCTCTCTCTTGTGCTGATCTCATCAGATCTTC 717
Db 758 GTCATTGAAGTGTGTTGTTAATCATGAACCCATGTCGCTGATGATTCATCAGATTTTC 817
QY 718 GCCGCGCAGCGCTACTCTCTTGTGTTGAATGCGAACAACGCGTGGCAACTACTTGGGTC 777
```


Db 818 GCTGCTCAACGATACTCGTTTCATCTCACTGCAAACTCAAACTGCTGATAATATTATGGATC 877
QY 778 CGCGCAACCCGAACTTCGACGGTTGGGTTGCGGGGGGATCACTCCGCCATCCTG 837
Db 878 CBTGCCAATCCTAACACGGACATACCGGGTTCGCTGGGGGTATAACACGGCGATCTG 937
QY 838 CGCTACCAAGCGCACAGTCGCGGAGCCCACTACGACCCAGACGACGTCGGTGATCCCG 897
Db 938 CGTTATTCTGGCGCCCTGTTGCTGATCGGTCACTACCCA---GACTTCTGCCAACCTT 994
QY 898 CTTATCGAGACGAACTTGCACCCCTCGCTCGCATCGCTGTGCTGGCAGCCCGACACCC 957
Db 995 CTACAGGAACAACGCTTGTCCGCGGTGAAATCCCGGTGCTCTGGAATGCAACTGCT 1054
QY 958 GGGGGGCTCGCAAGGCGCTCAACGCTCGCTTTAACTTCAACGCGCACCAACTCTTCATC 1017
Db 1055 AACGGCTAGATGTTGACTTGATCTGGTCTTATCATTTTGGAGGACGGTTCGAGATT 1114
QY 1018 AACACGGGACTTTACGCGCGCGGACCGTCCCGGTACTCTCCAGATTCTGAGCGGTGCG 1077
Db 1115 AAGGGGTATCCTTTGTACCCCTACAGTCCCTGTCTTACTTCAAAATTTCTCAGCGGAGCC 1174
QY 1078 CAGACGCAACAGACCTGCTCCCTGAGGCTCTGTCTACCGCTCCCGGCCCACTCCACC 1137
Db 1175 ACTACAGACCGCAACTTCTACCCAGTGGCTCTGTTTATACATTGCCCTTGAATTGGTC 1234
QY 1138 ATCAGATACAGCTGCCCGGACCGCTTGGCCCGGGTGCA---CGCACCCCTTCCAC 1194
Db 1235 ATCCAGTTGAGCTTTAATACGGTTGCAGTTGCAGCAGTTGGAGGTCTCTCATCCATCCAT 1294
QY 1195 CTGACGGGTACCGCTTCGGGTCGTTCCGAGCGCGGGAGCACCAGGTATACTACAC 1254
Db 1295 CTTACGGGACACATTTGACGTGGTCCGGAAGTCCCGGAAGTACCGAGTATACTATATC 1354
QY 1255 GACCCGATCTTCGCGACGCTGCTGAGCAGCGGCAACCGCCCGCGGCGACACGTCACG 1314
Db 1355 AACCTCCGCGAGGATGCTCTACTGTT-----GCAGTACTGACATGTAACC 1408
QY 1315 ATCCGCTTCAGACGGAACACCCCGGCGGTGTTCTCTACATGCCACATTCGACTTCCAC 1374
Db 1409 ATTGCTTTACTACTGATATGCTGGACCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1468
QY 1375 CTGACGCGGGCTTCGCGATCGTTTCGACAGAGGAGCTTCGCGACGTGAAGCGCGCAAC 1434
Db 1469 CTGGAAGCTGGTTTGTATGTTTTCGAGGATGACCGGACGTCGCGCGGTAAAT 1528
QY 1435 CCAGTTCCGAAGCGGTGCTGCGACCTGTGCGGATCTACGACGGGCTGAGCGAGGCTAAC 1494
Db 1529 CCGTCCCGACGCTTGGAAATCACTTTGCCCAACTATGATGCTTTGACCCCTGCACAA 1588
QY 1495 C 1495
Db 1589 C 1589

RESULT 15
AAT67137
ID AAT67137 standard; cDNA; 1170 BP.
XX
AC AAT67137;
XX
DT 22-JUL-1997 (first entry)
XX
DE Coprinus cinereus lcc2 partial cDNA.
XX
KW Benzenediol: oxygen oxidoreductase; laccase; lignin; Kraft pulp; dye;
KW fungus; polymerase chain reaction; papermaking; ss.
XX
OS Coprinus cinereus (strain IFO 8371).
XX
PN W09708325-A2.
XX

PD 06-MAR-1997.
XX
PF 20-AUG-1996; 96WO-US13728.
XX
PR 25-AUG-1995; 95US-0002800.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Brown KM, Halkier T, Kauppinen S, Yaver DS;
XX WPI; 1997-179282/16.
XX
XX New laccase from Coprinus strains - useful for polymerising lignin,
PT depolymerising Kraft pulp, oxidising dyes and their precursors, etc.
PT
XX Example 5; Page -: 62pp; English.
XX
CC The present sequence encodes a partial cDNA of lcc2, isolated from
CC Coprinus cinereus strain IFO 8371, starting in exon 3. The lcc2
CC polypeptide is used to polymerise a lignin or lignosulphate in solution;
CC for in situ depolymerisation of Kraft pulp; for oxidising dyes or their
CC precursors; particularly to prevent dye transfer between fabrics and in
CC hair dyeing) and for polymerising or oxidising phenolic compounds (e.g.
CC to precipitate phenolics from fruit juices to give a more stable
CC product). It can also be used for soil detoxification. Use of the
CC polypeptide avoids the need to use chlorine for lignin depolymerisation.
CC It has better activity than known laccases under the alkaline conditions
CC usually encountered in papermaking processes.
XX
SQ Sequence 1170 BP; 228 A; 384 C; 264 G; 294 T; 0 other;

Query Match 31.5%; Score 472.6; DB 18; Length 1170;
Best Local Similarity 65.0%; Pred. No. 1.9e-83;
Matches 770; Conservative 0; Mismatches 394; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGCTCTTCCAGGAGGACCACTGGCGCAGCAGCAGCGCTTGGTCAAC 249
Db 1 CACTGGCAGCGCTCTTCCAAAGGGGACTGCTGGGCTGATGGTCTGGCGTCAAC 60
QY 250 CAGTGCCTATTGTTCCGGGCATTTCTGTACCACTTCCATGTGCCGACGAGCA 309
Db 61 CAATGCCCTATTCCCGAGGCACTTCTTGTACAGTTCCAGGCTCTTAAACAAGCC 120
QY 310 GGAACGTTCTGGTACCACATCTCTCTACGCAATACGTGTGAGGGGTGCGAGGACCC 369
Db 121 GGTACTTCTGGTACCACCTCCCATCGCAATATGTCAGCGTTTGGCTGGGCT 180
QY 370 TTGCTGCTGTACGACCCCAAGGATCCGACGCGCGCTACGATGTGACAGGAGC 429
Db 181 ATGGTCTATATGACCCGATCGACCCACATCGCAACTTGTATGACATGACACGAGGCC 240
QY 430 ACGGTCTATCAGTTGACCGACTGTGTACACACCGCTCCCGGGTCTCGGTCCAGGTTCCCA 489
Db 241 ACGATCATTAAGCTCGCAGACTGTATCAGTCCCTGC---TCCCTCTGCAGGTTCTGTT 297
QY 490 CTGCGCGCGGACCGCAGGCTATCAATGGTCTTGGGGGGGTGGGCTCCATCCACCGCC 549
Db 298 CCCACCCAGATTCCAGCTTATACAGGTAAGGGCGGTATGCTGGCCCTTACCGTA 357
QY 550 GCGTCTGCTGTATCAACGTCACGACGCGGAAAGCGTACCGCTTCCGCTCTGTTTCGATC 609
Db 358 CTTCTCGGGTCAATTTCTGTAAACCCGAAACCGGAGTACCGGTTCCCGCTTGTTCCTT 417
QY 610 TCGTGGACCCGAACTACAGTTTACAGATCGAGGGGACAACTGTGACCGTATCGAGGTC 669
Db 418 TCATCGCATCTAATATGATTTCTCTCATCGTGGCATACCATGACTGTTATTGAGGTC 477
QY 670 GACGGTATCAACAGCAGCCTCTCTTGTGCTGACTCTATCCAGATCTTTCGCGCGCAGCC 729
Db 478 GACGGAGTTAAGCTTCAACCTCTGTTGTGCTGCTGATCGATCTTTCGAGGTCAGCGC 537
QY 730 TACTCCTTTGTTGAATGCAACCAACGTCGGCAACTACTTGGTCCGCGCAACCCG 789

[illegible]

Search completed: December 14, 2002, 05:19:26
Job time : 291 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 06:54:27 ; Search time 70 Seconds
(without alignments)
949.887 Million cell updates/sec

Title: US-09-786-960-2

Perfect score: 2669

Sequence: 1 AIGPVASLVANAPVSPDGF.....VPKAWSDLCPIYDGLSEANQ 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2669	100.0	499	21 AAY92248	Trametes versicolor
2	2669	100.0	499	23 ABB05377	Trametes versicolor
3	2656	99.5	499	19 AAW76308	Polyporus pinnatus
4	2656	99.5	499	19 AAW60876	Polyporus pinnatus
5	2656	99.5	519	17 AAR90722	Laccase-LCC2. Pol
6	2238	83.9	499	11 AAR05279	Amino acid sequenc
7	2238	83.9	499	11 AAR07068	Phenol oxidase (PO
8	2238	83.7	499	11 AAR07069	Phenol oxidase (PO
9	2201	82.5	499	19 AAW76295	Polyporus pinnatus
10	2201	82.5	499	19 AAW60875	Polyporus pinnatus

11	2194	82.2	499	19 AAW76296	Polyporus pinnatus
12	2194	82.2	520	17 AAR90721	Laccase-LCC1. Pol
13	2191	82.1	499	19 AAW76297	Polyporus pinnatus
14	2187	81.9	520	23 ABB7510	Trametes versicolor
15	2185	81.9	499	19 AAW76298	Polyporus pinnatus
16	2178	81.6	499	19 AAW76299	Polyporus pinnatus
17	2113	79.2	524	20 AAW92810	T. versicolor lacc
18	1917.5	71.8	527	17 AAR90725	Laccase-LCC5. Pol
19	1842	69.0	511	17 AAR90724	Laccase-LCC4. Pol
20	1772	66.4	512	17 AAR90723	Laccase-LCC3. Pol
21	1772	66.4	518	23 AAU96688	Lentinula edodes p
22	1748.5	65.5	533	21 AAY93952	Amino acid sequenc
23	1748.5	65.5	533	21 AAY93953	Amino acid sequenc
24	1716	64.3	548	13 AAR20735	Laccase enzyme. p
25	1716	64.3	548	19 AAW76309	Phlebia radiata la
26	1716	64.3	548	19 AAW60877	Phlebia radiata la
27	1704.5	63.9	517	18 AAW17975	Coprinus cinereus
28	1667.5	62.5	516	18 AAW17974	Coprinus cinereus
29	1598	59.9	518	19 AAW61387	Schizophyllum comm
30	1577.5	59.1	533	23 AAU96689	Lentinula edodes p
31	1533	57.4	539	18 AAW17973	Coprinus cinereus
32	1533	57.4	539	19 AAW76281	Coprinus cinereus
33	1533	57.4	539	19 AAW60874	Coprinus cinereus
34	1505	56.4	539	19 AAW76282	Coprinus cinereus
35	1477.5	55.4	505	23 AAU96690	Lentinula edodes p
36	1431.5	53.6	548	23 AAU96691	Lentinula edodes p
37	1178.5	44.2	529	19 AAW76310	Rhizoctonia solani
38	1178.5	44.2	529	19 AAW60878	Rhizoctonia solani
39	1178.5	44.2	529	21 AAY50728	R. solani laccase
40	1176.5	44.1	529	16 AAR72328	Laccase Kslac3. R
41	1169.5	43.8	529	18 AAW16301	Rhizoctonia solani
42	1000	37.5	599	19 AAW76311	Rhizoctonia solani
43	1000	37.5	599	19 AAW60879	Rhizoctonia solani
44	983	36.8	599	16 AAR72319	Laccase Kslac2 pro
45	930.5	34.9	572	19 AAW76312	Rhizoctonia solani

ALIGNMENTS

RESULT 1
AAY92248
ID AAY92248 standard; Protein; 499 AA.
XX AC AAY92248;
XX
XX
DT 10-AUG-2000 (first entry)
XX
XX Trametes versicolor laccase.
DE
XX Laccase; transgenic plant; large scale production; paper; pulp;
KW lignin; degradation; biosynthesis.
XX
XX Trametes versicolor.
OS
XX
PN WO200020615-A2.
XX
XX
PD 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23256.
XX
XX 05-OCT-1998; 98US-0103031.
XX
XX (PROD-) PRODIGENE INC.
XX Hood E, Howard J, Jilka J;
XX WPI; 2000-303793/26.
XX N-PSDB; AAA09191.
XX Industrial scale laccase production in recombinant corn and maize
XX plants to produce enzymes for use in the paper industry

Example 1; Page 17-19; 34pp; English.

PS The Trametes versicolor laccase gene can be used to create transgenic
XX plants which produce laccase at levels of about 0.01% or higher of the
CC total soluble protein of the plant. The transgenic plants may be used
CC for the large scale production of laccase enzymes. Laccase is mainly
CC used in the paper and pulp industry for breaking down lignin.
CC Conversely, laccase is also involved in lignin biosynthesis and the
CC formation of lignin polymers. It is therefore useful as a biological
CC adhesive for gluing wood (e.g. in the production of plywood, oriented
CC strand board, particle board and medium density fiberboard). Laccase
CC may also be used for catalyzing the oxidation of compounds such as
CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is
CC also used as a marker enzyme in enzyme immunoassays, for the oxidation
CC of steroids and the synthesis of vinblastine (a cytostatic compound
CC used in treating malignant diseases).

XX Sequence 499 AA;

Query Match 100.0%; Score 2669; DB 21; Length 499;
Best Local Similarity 100.0%; Pred. No. 7.4e-218;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAPVSPDGFRLDAIVVNGVVPSPPLITGKGRFQLNVVDLTHNSMLKS 60
Db 1 AIGPVASLVANAPVSPDGFRLDAIVVNGVVPSPPLITGKGRFQLNVVDLTHNSMLKS 60
Qy 61 TSIHWGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 61 TSIHWGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Qy 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Db 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Qy 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Qy 241 AQRYSVFLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAPETTTQTTSVIPL 300
Db 241 AQRYSVFLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAPETTTQTTSVIPL 300
Qy 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
Db 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
Qy 421 IFRDVVSTGTGAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVVSTGTGAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 2
ABB05377

ID ABB05377 standard; Protein; 499 AA.

XX

AC ABB05377;

XX

DT 09-APR-2002 (first entry)

XX Trametes versicolor laccase I protein.

DE Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;

XX copper; metal cofactor; plant.

KW

XX

OS Trametes versicolor.

XX WO200196543-A2.

PN

XX 20-DEC-2001.

XX

XX 14-JUN-2001; 2001WO-US19174.

PF

XX 15-JUN-2000; 2000US-211732P.

XX

PR (PROD-) PRODIGENE INC.

PA (GEMV) GENENCOR INC.

XX

PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;

XX Woodard S;

XX WPI: 2002-090204/12.

DR N-PSDB; ABA92910.

XX

XX Improving recovery of active enzyme e.g. laccase, which requires

XX transitional metal cofactor e.g. copper for activity, from a plant, by

PT introducing plant nucleotide sequences encoding the enzyme and exposing

PT it to cofactor.

XX

XX Example 1; Fig 1A-C; 81pp; English.

XX

XX The present invention describes a method for improving the recovery of

CC an active enzyme from a plant where the enzyme requires a transitional

CC metal cofactor for activity. The method comprises introducing into the

CC plant nucleotide sequences encoding the enzyme and exposing the enzyme

CC to the metal cofactor. The method is useful for improving recovery of

CC an active enzyme which requires a transitional metal cofactor for activity,

CC preferably for improving recovery of active laccase which requires

CC copper for activity. The method can be used for improving recovery of

CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires

CC zinc, nickel, cobalt or manganese for activity, where the method further

CC comprises adding bicarbonate ion salt. The present sequence represents

CC the fungal Trametes versicolor laccase I enzyme. Laccases are also called

CC blue copper oxidases and use copper to accept and donate electrons in

CC the oxidation and reduction of substrates.

XX

XX Sequence 499 AA;

XX

XX Query Match 100.0%; Score 2669; DB 23; Length 499;

XX Best Local Similarity 100.0%; Pred. No. 7.4e-218;

XX Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAPVSPDGFRLDAIVVNGVVPSPPLITGKGRFQLNVVDLTHNSMLKS 60
Db 1 AIGPVASLVANAPVSPDGFRLDAIVVNGVVPSPPLITGKGRFQLNVVDLTHNSMLKS 60
Qy 61 TSIHWGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 61 TSIHWGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Qy 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Db 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Qy 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Qy 241 AQRYSVFLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAPETTTQTTSVIPL 300
Db 241 AQRYSVFLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAPETTTQTTSVIPL 300
Qy 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNENGFNFINNATFTPTVPVLLQILSGAQ 360
Db 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNENGFNFINNATFTPTVPVLLQILSGAQ 360
Qy 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
Db 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420

Db 361 TAQDLLPAGSVYPLPAHSTIETITLPATLAPGAPHPFHLGHAFVAVRSAGSTTYYNDP 420
QY 421 IFRDVSSTGTPAAGDNVIRFQTDNPGPWFHLCHIDFHLDAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVSSTGTPAAGDNVIRFQTDNPGPWFHLCHIDFHLDAGFAIVFAEDVADVKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 3
AAW76308
ID AAW76308 standard; protein; 499 AA.
XX
AC AAW76308;
XX
DT 08-JAN-1999 (first entry)
XX
DE Polyporus pinsitus (II) laccase protein.
XX
KW Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW denim; lignin modification; paper strengthening; phenol polymerisation;
KW hair dye; waste water treatment.
XX
OS Polyporus pinsitus.
PN W09838287-A1.
XX
PD 03-SEP-1998.
XX
PF 23-FEB-1998; 98WO-DK00070.
XX
PR 28-FEB-1997; 97DK-000022.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Svendsen A, Xu F;
XX
DR WPI; 1998-495393/42.
XX
PT New variants of Coprinus and related laccases with increased
PT oxidation potential - or altered pH optimum, or mediator or
PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
PT dye transfer and in bleaching textiles, especially as detergent
PT additive
XX
PS Disclosure; Pages 120-122; 147pp; English.
XX
CC The present sequence represents a laccase protein. The specification
CC describes active laccase variants (see AAW76282, AAW76296-99 and
CC AAW76316-17) having increased oxidation potential, altered pH optimum,
CC altered mediator and/or altered oxygen/hydroxide ion pathway. The
CC laccase variants are used specifically to oxidise substrates, to
CC inhibit dye transfer, and for bleaching textiles, specifically denim.
CC They can also be used for lignin modification, strengthening paper,
CC polymerisation of phenols, dyeing of hair and textiles and waste
CC water treatment.
XX
SQ Sequence 499 AA;

Query Match 99.5%; Score 2656; DB 19; Length 499;
Best Local Similarity 99.4%; Pred. No. 9.4e-217;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 AIGPVASLVWANAPVSPDGLRDAIVNGVVPSPPLITCKGDRFOLNVVDITLNHSMUKS 60
QY 61 TSIHWHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 61 TSIHWHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120

QY 121 RGPFFVVPKDPHASRYDVDNESTVITLTDWYHTAARLGPFRPLGADATLINGLRSAST 180
Db 121 RGPFFVVPKDPHASRYDVDNESTVITLTDWYHTAARLGPFRPLGADATLINGLRSAST 180
QY 181 PTAALAVINVOHGKRYRFLSVISCDPNYTFSIDGHNLTIVIEVDGINSOPLLVDSIQIFA 240
Db 181 PTAALAVINVOHGKRYRFLSVISCDPNYTFSIDGHNLTIVIEVDGINSOPLLVDSIQIFA 240
QY 241 AQRYSFVLNANOTGVNWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
Db 241 AQRYSFVLNANOTGVNWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGFNFFINNATFTPTVPVLLQLISGAQ 360
Db 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGFNFFINNATFTPTVPVLLQLISGAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIETITLPATLAPGAPHPFHLGHAFVAVRSAGSTTYYNDP 420
Db 361 TAQDLLPAGSVYPLPAHSTIETITLPATLAPGAPHPFHLGHAFVAVRSAGSTTYYNDP 420
QY 421 IFRDVSSTGTPAAGDNVIRFQTDNPGPWFHLCHIDFHLDAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVSSTGTPAAGDNVIRFQTDNPGPWFHLCHIDFHLDAGFAIVFAEDVADVKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 4
AAW60876
ID AAW60876 standard; Protein; 499 AA.
XX
AC AAW60876;
XX
DT 09-NOV-1998 (first entry)
XX
DE Polyporus pinsitus (II) laccase.
XX
KW Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;
KW detergent; bleaching.
XX
OS Polyporus pinsitus.
XX
FH Key Location/Qualifiers
FT Misc-difference 107 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe or His) at this position"
FT
FT Misc-difference 116 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 108 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 152 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 57 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe, Val, Ile, Leu or Gln) at this
FT position"
XX
PN W09827198-A1.

XX 25-JUN-1998.
XX 16-DEC-1997; 97WO-DK00571.
XX 08-SEP-1997; 97DK-0001021.
XX 19-DEC-1996; 96DK-0001449.
XX (NOVO) NOVO-NORDISK AS.
XX Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
XX Svendsen A;
XX WPI; 1998-362768/31.
XX New laccase variants with improved stability - having amino acid
XX changes based on Coprinus laccase structure, used for e.g.
XX oxidation, dye transfer inhibition or bleaching
XX
XX Claim 11; 143-145; 168pp; English.
XX This is a laccase enzyme of Polyporus pinsitus. The invention
XX relates to the design of new variants of Coprinus-like laccases
XX (see AA60874-79, AA60925 and AA62501-03); the P. pinsitus laccase
XX (II) shows 73.8% homology to C. cinereus laccase. The modifications
XX are based on the previously unknown three-dimensional structure of
XX C. cinereus laccase. Amino acid residues identified as being
XX important to protein stability are identified and altered to
XX improve stability. The variants are typically obtained by
XX mutagenesis of laccase DNA and expression in a host cell. Variants
XX are preferably modified within 15 (especially 10 or 5) Angstrom
XX of a copper ion in the three-dimensional structure of the laccase.
XX For P. pinsitus (II) laccase variants, preferred substitutions are
XX one or more of W107F/H, Y116F, Y108F, Y152F or M57E/V/L/Q. The
XX stabilised laccase variants can be used in detergent additives, for
XX dye transfer inhibition in detergents, in bleaching of textiles (in
XX particular denim), for lignin modification, paper strengthening,
XX phenol polymerisation, hair dyeing and in waste water treatment.
XX
XX SQ Sequence 499 AA;
Query Match 99.5%; Score 2656; DB 19; Length 499;
Best Local Similarity 99.4%; Pred. No. 9.4e-217;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPVSPDGLRDAIVVGVPSPLITGKGRFQLNVVDLTNHSMLKS 60
DB 1 AIGPVASLVVANAPVSPDGLRDAIVVGVPSPLITGKGRFQLNVVDLTNHSMLKS 60
QY 61 TSIHWGFFQAGTNWAGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSIHWGFFQAGTNWAGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPFLGADATLNLGHSAST 180
DB 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPFLGADATLNLGHSAST 180
QY 181 PTAALAVINVQHGKRYFRVLVSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 181 PTAALAVINVQHGKRYFRVLVSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNFTGVPAGGINSAILRYQAGPAEPTTTQTTSTVIPL 300
DB 241 AQRYSFVLNANQTVGNVWRANFNFTGVPAGGINSAILRYQAGPAEPTTTQTTSTVIPL 300
QY 301 IETNLHPLARMPVPGSTPGCVGDKALNLAENFNFTGVPAGGINSAILRYQAGPAEPTTTQTTSTVIPL 360
DB 301 IETNLHPLARMPVPGSTPGCVGDKALNLAENFNFTGVPAGGINSAILRYQAGPAEPTTTQTTSTVIPL 360
QY 361 TAODLLPAGSVYPLPAHSTTEITLPTALAPGAPHPFLHGHAFVAVRSAGSTTYNNDP 420
DB 361 TAODLLPAGSVYPLPAHSTTEITLPTALAPGAPHPFLHGHAFVAVRSAGSTTYNNDP 420

QY 421 IFRDVYSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLHDAGFAIVFAEDVADVKAANPV 480
DB 421 IFRDVYSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLHDAGFAIVFAEDVADVKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PKAWSDLCPYDGLSEANQ 499
RESULT 5
AAR90722
ID AAR90722 standard; Protein; 519 AA.
XX
XX AAR90722;
XX
XX 07-APR-1996 (first entry)
XX
XX Laccase-LCC2.
DE
KW Laccase-LCC2; Polyporus pinsitus; Trametes villosa;
KW signal peptide; Aspergillus; cDNA probe; Escherichia coli;
KW plasmid pDSY19; lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
XX cloning; basidiomycetes.
OS Polyporus pinsitus.
OS Trametes villosa.
FH Key Location/Qualifiers
FT Peptide 1..20 /note= "Signal peptide"
XX
XX WO9600290-A1.
XX 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
XX 15-MAY-1995; 95US-0441147.
XX 24-JUN-1994; 94US-0265534.
XX
XX (NOVO) NOVO NORDISK BIOTECH INC.
XX (NOVO) NOVO-NORDISK AS.
XX
XX Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
XX WPI; 1996-068874/07.
XX N-PSDB; AAT15599.
XX
XX DNA constructs for expression of Polyporus laccase enzymes - for use
XX in e.g. lignin manipulation, juice mfr., phenol polymerisation and
XX phenol resin prodn
XX
XX Claim 5; Page 65-67; 137pp; English.
XX
XX The sequence corresponds to laccase-LCC2 (pi 5.95) from Polyporus
XX pinsitus (Trametes villosa). A cDNA probe is obtained by
XX expression in Aspergillus oryzae, and used to screen a P. pinsitus
XX genomic library in Escherichia coli DH5-alpha, giving plasmid
XX pDSY19 (23GEN), with an 4-kb HindIII insert (NRRL B-21266).
XX Screening also results in isolation of genes encoding 4 other
XX laccases produced by P. pinsitus, LCC1 (AAR90721) and LCC3-LCC5
XX (AAR90723-R90725). The laccases may be used to polymerise lignin or
XX lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
XX precursors, in hair dye compositions, or to polymerise or oxidise
XX a phenolic or aniline compound. These new laccases are
XX well-expressed in Aspergillus spp. (with vector integration in the
XX genome), in contrast to previous basidiomycete laccases, which give
XX low yields of recombinant enzyme.
XX
XX Sequence 519 AA;
Query Match 99.5%; Score 2656; DB 17; Length 519;

Best Local Similarity 99.4%; Pred. No. 1e-216;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGLRDAIVVNGVVPSPITGKKGRFQNLVVDITLNHSMKLS 60
|||||
Db 21 AIGPVASLVVANAPVSPDGLRDAIVVNGVVPSPITGKKGRFQNLVVDITLNHSMKLS 80
|||||

QY 61 TSIHWHGFFQAGTNWADGPAFVNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSYQYCDGL 120
|||||
Db 81 TSIHWHGFFQAGTNWADGPAFVNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSYQYCDGL 140
|||||

QY 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLGRSAST 180
|||||
Db 141 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLGRSAST 200
|||||

QY 181 PTAALAVINVQHGKRYRFRFLVSLISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFA 240
|||||
Db 201 PTAALAVINVQHGKRYRFRFLVSLISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFA 260
|||||

QY 241 AQRYSEVLNANQTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
|||||
Db 261 AQRYSEVLNANQTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
|||||

QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGTFFINNATFTPTTPVPLLQILSGAQ 360
|||||
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGTFFINNATFTPTTPVPLLQILSGAQ 380
|||||

QY 361 TAQDLLPAGSVVPLPAHSTIETLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNYNDP 420
|||||
Db 381 TAQDLLPAGSVVPLPAHSTIETLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNYNDP 440
|||||

QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFADVDVADVKAANPV 480
|||||
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFADVDVADVKAANPV 500
|||||

QY 481 PKAWSDLCPYDGLSEANQ 499
|||||
Db 501 PKAWSDLCPYDGLSEANQ 519
|||||

RESULT 6
AAR05279
ID AAR05279 standard; protein; 499 AA.
XX
AC AAR05279;
XX
DT 18-AUG-1990 (first entry)
XX
DE Amino acid sequence of phenol oxidase (PO).
XX
KW Phenol oxidase (PO); biological pulping; enzyme.
XX
PN JP02005877-A.
XX
PD 10-JAN-1990.
XX
PF 16-JUN-1988; 88JP-0149103.
XX
PR 16-JUN-1988; 88JP-0149103.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-053914/08.
XX
DR N-PSDB; AAQ03366, AAN93367.
XX
PT Phenol oxidase gene - used for biological pulping, etc.
XX
PS Page 812-813; Fig 2; 14pp; Japanese.
XX
CC By knowing its total amino acid sequence, the part of it that is involved
CC in lignin decomposition can be isolated and applied to biological
CC pulping. It does not contaminate cellulose or hemicellulose and can be
CC used for biological pulping where lowering of pulp yield does not occur.
CC

CC It is very pure and it is useful as a biochemical or diagnostic reagent.
CC The same sequence is found in JO 2005-876-A.

XX SQ Sequence 499 AA;
Query Match 83.9%; Score 2238; DB 11; Length 499;
Best Local Similarity 81.6%; Pred. No. 2.9e-181;
Matches 407; Conservative 35; Mismatches 57; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGLRDAIVVNGVVPSPITGKKGRFQNLVVDITLNHSMKLS 60
|||||
Db 1 AIGPTADLTISNAEVSPPDGFARQAVVNVNTPGLVAGNKGDRFQNLVDNLNTHMTKLS 60
|||||

QY 61 TSIHWHGFFQAGTNWADGPAFVNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSYQYCDGL 120
|||||
Db 61 TSIHWHGFFQAGTNWADGPAFVNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSYQYCDGL 120
|||||

QY 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLGRSAST 180
|||||
Db 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLGRSAST 180
|||||

QY 181 PTAALAVINVQHGKRYRFRFLVSLISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFA 240
|||||
Db 181 TAADLAVINVTRKRYRFRFLVSLISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFA 240
|||||

QY 241 AQRYSEVLNANQTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
|||||
Db 241 AQRYSEVLNANQTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
|||||

QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGTFFINNATFTPTTPVPLLQILSGAQ 360
|||||
Db 301 NEVDLHPLATMAVPGSPVAGGVDTAINMAFNENGTFFINGASEVPTTPVPLLQILSGAQ 360
|||||

QY 361 TAQDLLPAGSVVPLPAHSTIETLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNYNDP 420
|||||
Db 361 NAQDILLPSGSVYSLPSNADIEISFPATAAAGAPHPFLHGHAFVAVRSAGSTTYNYNDP 420
|||||

QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFADVDVADVKAANPV 480
|||||
Db 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFADVDVADVKAANPV 480
|||||

QY 481 PKAWSDLCPYDGLSEANQ 499
|||||
Db 481 PKAWSDLCPYDGLSEANQ 499
|||||

RESULT 7
AAR07068
ID AAR07068 standard; protein; 499 AA.
XX
AC AAR07068;
XX
DT 03-FEB-1991 (first entry)
XX
DE Phenol oxidase (PO) gene product.
XX
KW Paper pulping.
XX
PN JP02027986-A.
XX
PD 30-JAN-1990.
XX
PF 15-JUL-1988; 88JP-0175236.
XX
PR 15-JUL-1988; 88JP-0175236.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-32326/43.
XX
DR N-PSDB; AAQ03571.
XX
PT New phenol oxidase gene - has DNA encoding specified sequence of
PT 499 amino acid(s)

```
XX Claim 1; Page 559; 15pp; Japanese.
XX PO is useful in biological paper pulping and bleaching.
XX
XX Sequence 499 AA;
XX
Query Match 83.9%; Score 2238; DB 11; Length 499;
Best Local Similarity 81.6%; Pred. No. 2.9e-181;
Matches 407; Conservative 35; Mismatches 57; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPSPDGFELRDAIVVGVVPSPLITGKGRFQLNVVDLTNNHSLKLS 60
DB 1 AIGPTADLTISNAEVSDFGARQAVVNNVTPGLVAGNKGDRFQLNVDLTNNHSLKLS 60
QY 61 TSHHGWFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSHHGWFFQAGTNWADGPAFVNOCPITSSGHSFLYDFQVDPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPRKDPHASRYDVNDNESTVITLTQWYHTAARLGRPRPLGADATLNLGRSAST 180
DB 121 RGFVVYDPRNDPHASLYDVNDNDTVINLADWYHTAAKLGPAFPLGADATLNLGRSPST 180
QY 181 PTAALAVINVQHGKRYRFRFLVSLSCDPNHTFSIDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 181 TAADLAVINVTKGRYRFRFLVSLSCDPNHTFSIDGHDLTIEVDINSQPLVVDSTQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNGVGFAGGINSAILRYQCAPVAEPTTTQTSVIPL 300
DB 241 AQRYSFVLNADQVGNVWRANFNGVGFAGGINSAILRYDQADPVEPTTTQTTKPL 300
QY 301 IETNLHPLARMPVPGSPTPGGVDKALNLAFFNNGTFFINNAFTPTPTVPLLIISGAQ 360
DB 301 NEVDLHPLATMAYPGSPVAGVDTAIINWAFNNGTFFINGASFVPTVPLLIISGAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATAPAGPHPHLHGHAFAVVRSGSTTYNNDP 420
DB 361 NAQDLLPSGSVYSLPSNADIEISFPATAAAGPHPHLHGHAFAVVRSGSTVYNDNP 420
QY 421 IFRDVVSTGTPAAGDNVTIRFQDNPGFWFLHCHIDHLDAGFAIVFAEDVADVKAANPV 480
DB 421 IFRDVVSTGTPAAGDNVTIRFQDNPGFWFLHCHIDHLDAGFAIVFAEDIPDVASANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PQAWSDLCPYDALDVNDQ 499
RESULT 8
AAR07069
ID AAR07069 standard; protein; 499 AA.
AC AAR07069;
XX
XX 03-FEB-1991 (first entry)
XX
XX Phenol oxidase (PO) gene product.
XX
XX Paper pulping.
XX
XX JP02027986-A.
XX
XX 30-JAN-1990.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX (OJIP ) OJI PAPER KK.
XX
XX WPI; 1990-323326/43.
XX
XX N-PSDB; AAQ03572.
XX
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PT New phenol oxidase gene - has DNA encoding specified sequence of
PT 499 aminoacid(s)
XX
XX Claim 1; Page 559; 15pp; Japanese.
XX
XX PO is useful in biological paper pulping and bleaching.
XX
XX Sequence 499 AA;
XX
Query Match 83.7%; Score 2233; DB 11; Length 499;
Best Local Similarity 81.4%; Pred. No. 7.6e-181;
Matches 406; Conservative 35; Mismatches 58; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPSPDGFELRDAIVVGVVPSPLITGKGRFQLNVVDLTNNHSLKLS 60
DB 1 AIGPTADLTISNAEVSDFGARQAVVNNVTPGLVAGNKGDRFQLNVDLTNNHSLKLS 60
QY 61 TSHHGWFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSHHGWFFQAGTNWADGPAFVNOCPITSSGHSFLYDFQVDPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPRKDPHASRYDVNDNESTVITLTQWYHTAARLGRPRPLGADATLNLGRSAST 180
DB 121 RGFVVYDPRNDPHASLYDVNDNDTVINLADWYHTAAKLGPAFPLGADATLNLGRSPST 180
QY 181 PTAALAVINVQHGKRYRFRFLVSLSCDPNHTFSIDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 181 TAADLAVINVTKGRYRFRFLVSLSCDPNHTFSIDGHDLTIEVDINSQPLVVDSTQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNGVGFAGGINSAILRYQCAPVAEPTTTQTSVIPL 300
DB 241 AQRYSFVLNADQVGNVWRANFNGVGFAGGINSAILRYDQADPVEPTTTQTTKPL 300
QY 301 IETNLHPLARMPVPGSPTPGGVDKALNLAFFNNGTFFINNAFTPTPTVPLLIISGAQ 360
DB 301 NEVDLHPLATMAYPGSPVAGVDTAIINWAFNNGTFFINGASFVPTVPLLIISGAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATAPAGPHPHLHGHAFAVVRSGSTTYNNDP 420
DB 361 NAQDLLPSGSVYSLPSNADIEISFPATAAAGPHPHLHGHAFAVVRSGSTVYNDNP 420
QY 421 IFRDVVSTGTPAAGDNVTIRFQDNPGFWFLHCHIDHLDAGFAIVFAEDVADVKAANPV 480
DB 421 IFRDVVSTGTPAAGDNVTIRFQDNPGFWFLHCHIDHLDAGFAIVFAEDIPDVASANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PQAWSDLCPYDALDVNDQ 499
RESULT 9
AAW76295
ID AAW76295 standard; protein; 499 AA.
XX
XX AAW76295;
XX
XX 08-JAN-1999 (first entry)
XX
XX Polyporus pinsitus (I) laccase protein.
XX
XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
XX denim; lignin modification; paper strengthening; phenol polymerisation;
XX hair dye; waste water treatment.
XX
XX Polyporus pinsitus.
XX
XX WO9838287-A1.
XX
XX 03-SEP-1998.
XX
XX 23-FEB-1998; 98WO-DK00070.
XX
XX 28-FEB-1997; 97DK-0000222.
XX
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XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Svendsen A, Xu F;
XX WPI; 1998-495393/42.
XX New variants of Coprinus and related laccases with increased
XX oxidation potential - or altered pH optimum, or mediator or
XX oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
XX dye transfer and in bleaching textiles, especially as detergent
XX additive
XX Disclosure; Pages 119-120; 147pp; English.
XX
XX The present sequence represents a laccase protein. The specification
XX describes active laccase variants (see AAW76282, AAW76296-99 and
XX AAW76316-17) having increased oxidation potential, altered pH optimum,
XX altered mediator and/or altered oxygen/hydroxide ion pathway. The
XX laccase variants are used specifically to oxidise substrates, to
XX inhibit dye transfer, and for bleaching textiles, specifically denim.
XX They can also be used for lignin modification, strengthening paper,
XX polymerisation of phenols, dyeing of hair and textiles and waste
XX water treatment.
XX
XX Sequence 499 AA;
SQ
Query Match 82.5%; Score 2201; DB 19; Length 499;
Best Local Similarity 80.1%; Pred. No. 3.9e-178;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
QY 2 IGPVSLVYANAVSPDGLRDAIVVNGVYVPSPLITKGGDRFQLNVVDLTNHSMLKST 61
Db 2 IGPVADLTITNAASVDPGFSRQAVVNGTGPCPLITNGMDRFQLNVIDLNHTMLKST 61
QY 62 STHWGFQAGTNYADGAFVNOCTIASHSELYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 STHWGFQAGTNYADGAFVNOCTIASHSELYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
QY 122 GPFVYDPRKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLSASPT 181
Db 122 GPFVYDPRNDPAADLYVDNDTDTVITLVDWYHVAALGPAPFLGADATLNGKSPST 181
QY 182 TAAIAVINQHKRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIOIFAA 241
Db 182 TADLSVISVTPGKRYRFRRLVSLSCDPNTFTSIDGHNMTIETDSINTAPLVVDSIOIFAA 241
QY 242 QRYSFVLNANQTVGNWVRANPNFTGVGFAGGINSAILRYOCAPVAEPTTOTTSTVPLI 301
Db 242 QRYSFVLEANQAVDNYWVRANPNFNGVFTGGINSAILRYDGAAVEPTTOTTSTAPLN 301
QY 302 ETNLHPLAMPVPGSPTPGGVKALNLAFFNENGTNFTFNNATFTPTPVLLQLILSGAQT 361
Db 302 EYNLHPLVTTAVPGSPVAGGVDLANMAFNENGTNFTFNGASFTPTPVLLQLIISGAQN 361
QY 362 AODLLPAGSVYPLPAHSITETITLPATAPAGPHFHLGHAFVAVRSAGSTTYNNDPI 421
Db 362 AODLLPSSGVSLPSNADIEISFPAATAAGAPGPHFHLGHAFVAVRSAGSTTYNNDPI 421
QY 422 FRDVTSTGTPAAGDNVTIRFQDNPFGPWFHLCHIDHLDAGFAIVFAEDVADVKAANPVP 481
Db 422 FRDVTSTGTPAAGDNVTIRFQDNPFGPWFHLCHIDHLDAGFAIVFAEDVADVKAANPVP 481
QY 482 KAWSLCPIYDGLSEANQ 499
Db 482 QAWSLCPTDYALDPSDQ 499
RESULT 10
AAW60875
ID AAW60875 standard; Protein; 499 AA.
XX
XX AAW60875;
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```
XX DT 09-NOV-1998 (first entry)
XX XX Polyporus pinsitus (I) laccase.
XX KW Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;
XX KW detergent; bleaching.
XX OS Polyporus pinsitus.
XX XX Key Location/Qualifiers
XX FT Misc-difference 107 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe or His) at this position"
XX FT Misc-difference 116 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe) at this position"
XX FT Misc-difference 108 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe) at this position"
XX FT Misc-difference 152 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe) at this position"
XX FT Misc-difference 57 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe, Val, Ile, Leu or Gln) at this
XX FT position"
XX FT Misc-difference 328 /note= "variant may have Ala, Val, Leu, Ile, Pro,
XX FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
XX FT Gln, Asp, Glu, Lys, Arg or His (preferably
XX FT Phe, Val, Ile, Leu or Gln) at this
XX FT position"
XX PN WO9827198-A1.
XX XX 25-JUN-1998.
XX XX 16-DEC-1997; 97WO-DK00571.
XX PR 08-SEP-1997; 97DK-0001021.
XX PR 19-DEC-1996; 96DK-0001449.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Cherry JR, Federsen AH, Rasmussen G, Schneider P;
XX PI Svendsen A;
XX XX WPI; 1998-362768/31.
XX XX New laccase variants with improved stability - having amino acid
XX changes based on Coprinus laccase structure, used for e.g.
XX FT oxidation, dye transfer inhibition or bleaching
XX PS Claim 10; 142-143; 168pp; English.
XX CC This is a laccase enzyme of Polyporus pinsitus. The invention
XX relates to the design of new variants of Coprinus-like laccases
XX (see AAW60874-79, AAW60925 and AAW62501-03); the P. pinsitus laccase (I)
XX shows 74.4% homology to C. cinereus laccase. The modifications are
XX based on the previously unknown three-dimensional structure of
XX C. cinereus laccase. Amino acid residues identified as being
XX important to protein stability are identified and altered to
```

CC improve stability. The variants are typically obtained by
 CC mutagenesis of lacase DNA and expression in a host cell. Variants
 CC are preferably modified within 15 (especially 10 or 5) Angstrom
 CC of a copper ion in the three-dimensional structure of the lacase.
 CC For p. pinsitus (I) lacase variants, preferred substitutions are
 CC one or more of W107F/H, Y116F, Y108F, Y152F, M57F/V/I/L/Q or
 CC M328F/V/I/L/Q (claimed). The stabilised lacase variants can be
 CC used in detergent additives, for dye transfer inhibition in
 CC detergents, in bleaching of textiles (in particular denim), for
 CC lignin modification, paper strengthening, phenol polymerisation,
 CC hair dyeing and in waste water treatment.

XX SQ Sequence 499 AA;

Query Match 82.5%; Score 2201; DB 19; Length 499;
 Best Local Similarity 80.1%; Pred. No. 3.9e-178;
 Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;

QY 2 IGPVAVSLVWVAPVSPDGLRDAIVWVGVPSPLITGKGRFQNLVVDVLTNHSMLKST 61
 DB 2 IGPVADLTITNAAVSPDGFSRQAVVNGGTPGLITGNMGDRFQNLVVDVLTNHSMLKST 61

QY 62 SIHHGFFQAGTNWADGPAFVWQCPVQASGHSFLYDFHVPDQAGTFWYHSLSTQYCDGLR 121
 DB 62 SIHHGFFQAGTNWADGPAFVWQCPVQASGHSFLYDFHVPDQAGTFWYHSLSTQYCDGLR 121

QY 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181
 DB 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181

QY 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181
 DB 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181

QY 182 TAALAVINVQHGKRYRFLVSLSCDPNYTFSIDGHNLTIVIEVDGINSQPLVDSIQIFAA 241
 DB 182 TADLSVLSVTPGKRYRFLVSLSCDPNYTFSIDGHNLTIVIEVDGINSQPLVDSIQIFAA 241

QY 302 ETNLHPLARMPVPGSPGPGVDKALNLAFAFNFTGNGFNFTGNGFNFTGNGFNFTGNGFNFT 361
 DB 302 EVNLHPLVTVAPGSPVAGVDLAINMAFNFTGNGFNFTGNGFNFTGNGFNFTGNGFNFT 361

QY 362 AQDLLPAGSVYPLPAHSTIETLTPALAPGAPHPFLHGHAFVAVRSAGSTTYNYNDPI 421
 DB 362 AQDLLPAGSVYPLPAHSTIETLTPALAPGAPHPFLHGHAFVAVRSAGSTTYNYNDPI 421

QY 422 FRDVSSTGTPAAGDNVTRFOTDNPFGWFLCHIDFHLDAFAIVFAEDVADVKAANPVP 481
 DB 422 FRDVSSTGTPAAGDNVTRFOTDNPFGWFLCHIDFHLDAFAIVFAEDVADVKAANPVP 481

QY 482 KAWSDLCPYDGLSEANO 499
 DB 482 QAWSDLCPYDGLSEANO 499

RESULT 11

AAW76296
 ID AAW76296 standard; protein; 499 AA.

XX AC AAW76296;

XX DT 08-JAN-1999 (first entry)

XX DE Polyporus pinsitus (I) lacase variant protein.

XX KW Lacase; variant; oxidation; dye transfer inhibition; bleaching;
 KW denim; lignin modification; paper strengthening; phenol polymerisation;
 KW hair dye; waste water treatment.

XX OS Synthetic.

XX OS Polyporus pinsitus.

XX FH Key Location/Qualifiers

FT Misc-difference 390 /label= A390X
 FT /note= "X is optionally Val, pro, Leu, Ile, Phe,
 FT Tyr or Trp"
 FT Misc-difference 392 /label= G392X
 FT /note= "X is optionally Ala, Val, pro, Leu, Ile, Phe,
 FT Tyr or Trp"
 FT Misc-difference 460 /label= E460D
 FT /note= "optional"
 XX

PN W09838287-A1.
 XX
 XX 03-SEP-1998.
 XX
 XX 23-FEB-1998; 98WO-DK00070.
 XX
 XX 28-FEB-1997; 97DK-0000222.
 XX (NOVO) NOVO-NORDISK AS.
 XX
 XX Svendsen A, Xu F;
 XX
 XX WPI; 1998-495393/42.
 XX
 XX New variants of Coprinus and related laccases with increased
 XX oxidation potential - or altered pH optimum, or mediator or
 XX oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
 XX dye transfer and in bleaching textiles, especially as detergent
 XX additive
 XX
 XX Claim 11; Page -; 147pp; English.

CC The present sequence represents a mutant lacase protein. The
 CC specification describes active lacase variants (see AAW76282,
 CC AAW76296-99 and AAW76316-17) having increased oxidation potential,
 CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide
 CC ion pathway. The lacase variants are used specifically to oxidise
 CC substrates, to inhibit dye transfer, and for bleaching textiles,
 CC specifically denim. They can also be used for lignin modification,
 CC strengthening paper, polymerisation of phenols, dyeing of hair and
 CC textiles and waste water treatment.
 CC
 CC note: the present sequence does not appear in the specification; it was
 CC constructed using information provided.

XX SQ Sequence 499 AA;

Query Match 82.2%; Score 2194; DB 19; Length 499;
 Best Local Similarity 79.9%; Pred. No. 1.5e-177;

Matches 398; Conservative 34; Mismatches 66; Indels 0; Gaps 0;

QY 2 IGPVAVSLVWVAPVSPDGLRDAIVWVGVPSPLITGKGRFQNLVVDVLTNHSMLKST 61
 DB 2 IGPVADLTITNAAVSPDGFSRQAVVNGGTPGLITGNMGDRFQNLVVDVLTNHSMLKST 61

QY 62 SIHHGFFQAGTNWADGPAFVWQCPVQASGHSFLYDFHVPDQAGTFWYHSLSTQYCDGLR 121
 DB 62 SIHHGFFQAGTNWADGPAFVWQCPVQASGHSFLYDFHVPDQAGTFWYHSLSTQYCDGLR 121

QY 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181
 DB 122 GPFVYVDPKDPHASYRDVNDNESTVITLTDWYHTAARLGPFPGLGADATLNGLSASSTP 181

QY 182 TAALAVINVQHGKRYRFLVSLSCDPNYTFSIDGHNLTIVIEVDGINSQPLVDSIQIFAA 241
 DB 182 TADLSVLSVTPGKRYRFLVSLSCDPNYTFSIDGHNLTIVIEVDGINSQPLVDSIQIFAA 241

QY 242 QRYSFVLNANQTVGNVWRANPNFTGVGAGINSAILRYOGAPVAEPTTTQTTSVPLI 301
 DB 242 QRYSFVLEANOQVDNYWIRANPNFTGVGAGINSAILRYOGAPVAEPTTTQTTSVPLI 301

QY 302 ETNLHPLARMPVPGSPGPGVDKALNLAFAFNFTGNGFNFTGNGFNFTGNGFNFTGNGFNFT 361

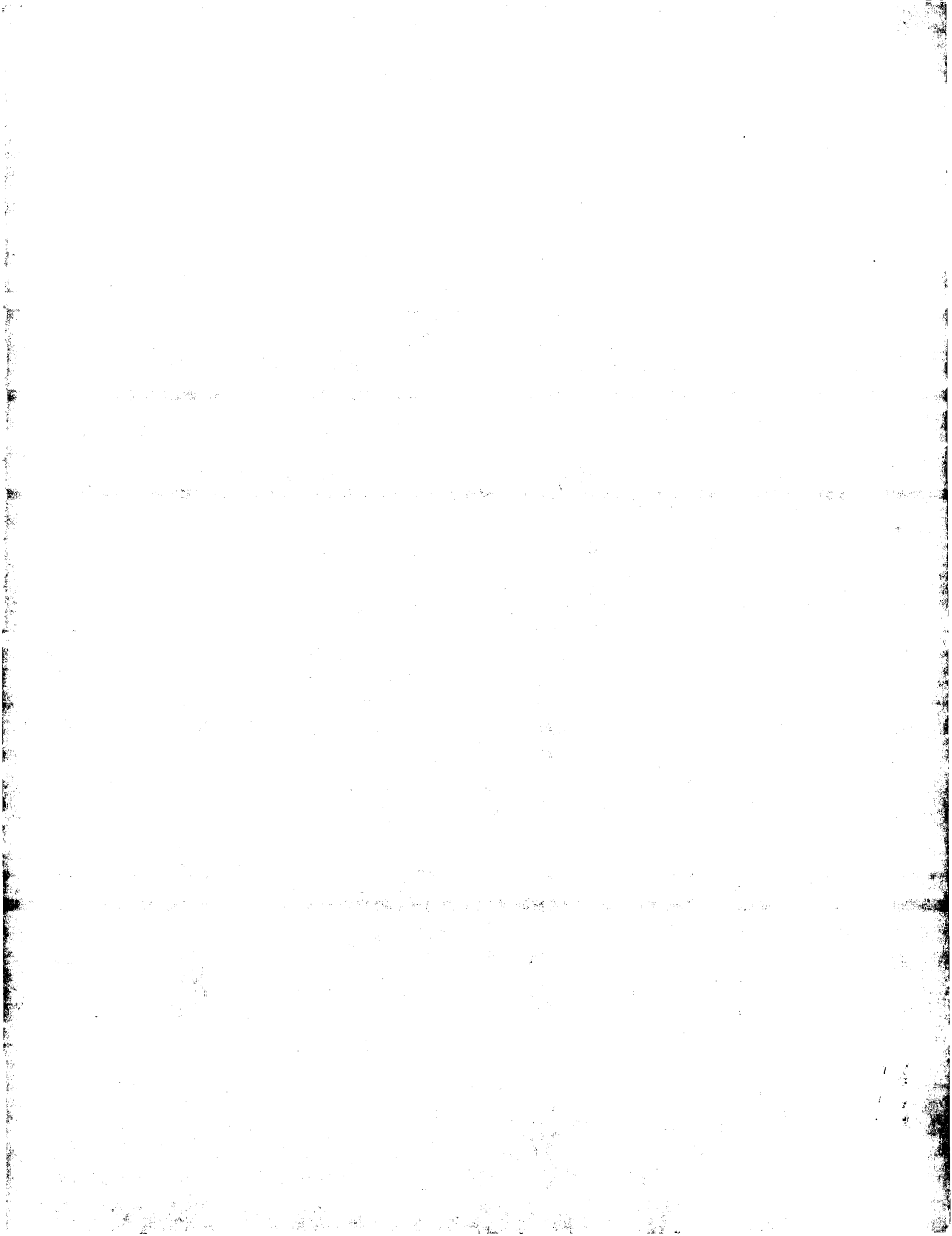
Db	302	EVNLHPLVTVAFSGPVAGVDUAINMAFNFTNFINGASFTPTVPVLQIIISGAON	361
Qy	362	AQDLLPAGSYVPLPAHSTIEITLPATALAGAPHPHFLHGFAFVYRSAGSTTYNDPI	421
Db	362	AQDLLPAGSYVPLPSNADIEISPTAAAXPXAPHPPHFLHGFAFVYRSAGSTVYNDPI	421
Qy	422	FRDVSVTGTPAAGDNVTIRFQTDNCPGFWFLCHIDPHLDGAFVAFVADVKANPVP	481
Db	422	FRDVSVTGTPAAGDNVTIRFQTDNCPGFWFLCHIDPHLDGAFVAFVADVPV	481
Qy	482	KAWSDLCPYDGLSEANQ	499
Db	482	QAWSDLCPYDALQSPD	499

QY 302 ETNLHPLARMVPGSTPGGVGDKALNLAFAFNFTGTFINNAFTPTPTVPLVLIISGAQT 361
Db 323 EVNLHPLVATVPGSPVAGGVDLAINMAFNFTGTFINNAFTPTPTVPLVLIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNDPI 421
Db 383 AQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPHLLGHAFVAVRSAGSTTYNDPI 442
QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDFHLDAFAIYFAEDVADVKAANPVP 481
Db 443 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDFHLDAFAIYFAEDVADVKAANPVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
Db 503 QAWSDLCPYDALDPSDQ 520

RESULT 15
AAW76299
ID AAW76299 standard; protein; 499 AA.
XX AC AAW76299;
XX DT 08-JAN-1999 (first entry)
XX DE Polyporus pinsitus (T) laccase variant protein.
XX KW Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW denim; lignin modification; paper strengthening; phenol polymerisation;
KW hair dye; waste water treatment.
XX OS Synthetic.
OS Polyporus pinsitus.
XX Key Location/Qualifiers
FH Misc-difference 80 /label= A80X
FT /note= "X is optionally Asp or Glu"
FT Misc-difference 81 /label= F81A
FT /note= "X is optionally Asp or Glu"
FT Misc-difference 112 /label= L112X
FT /note= "X is optionally Asp or Glu"
XX WO9838287-A1.
XX 03-SEP-1998.
XX 23-FEB-1998; 98WO-DK00070.
XX 28-FEB-1997; 97DK-0000222.
XX (NOVO) NOVO-NORDISK AS.
XX Svendsen A, Xu F;
XX WPI: 1998-495393/42.
XX New variants of Coprinus and related laccases with increased
XX oxidation potential - or altered pH optimum, or mediator or
XX oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
XX dye transfer and in bleaching textiles, especially as detergent
XX additive
PS Claim 14; Page -: 147pp; English.
XX The present sequence represents a mutant laccase protein. The
XX specification describes active laccase variants (see AAW76282,
XX AAW76296-99 and AAW76316-17) having increased oxidation potential,
XX altered pH optimum, altered mediator and/or altered oxygen/hydroxide
XX ion pathway. The laccase variants are used specifically to oxidise
XX substrates, to inhibit dye transfer, and for bleaching textiles,

CC specifically denim. They can also be used for lignin modification,
CC strengthening paper, polymerisation of phenols, dyeing of hair and
CC textiles and waste water treatment.
CC note: the present sequence does not appear in the specification; it was
CC constructed using information provided.
CC note: residue 260 is defined as Asn in the claims; however residue 260
CC of the wild type protein (AAW76295) is Arg"
XX SQ Sequence 499 AA;
Query Match 81.9%; Score 2185; DB 19; Length 499;
Best Local Similarity 79.5%; Pred. No. 9e-177;
Matches 396; Conservative 35; Mismatches 67; Indels 0; Gaps 0;
QY 2 IGPVASLVANAPVSPDGLRDAIVVNGVVPSPPLITGKGGDFQLNVVDLTNHSMLKST 61
Db 2 IGPVADLAITNAAVSPDGFSAVAVVNGTGPGLITGNMDRFLQNLNHTMLKST 61
QY 62 SIHWHGFTQAGTNWADGPAFVNOCPISAGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 121
Db 62 SIHWHGFTQAGTNWADGPAFVNOCPISAGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 121
QY 122 GPFVYDPAKPHASRYDVNDNESTVITLTDWYHTAARLGPFPPLGADATLNGRSGASTP 181
Db 122 GPFVYDPAADLYDVNDNDTITLVDMYHVAALGPFPPLGADATLNGRSGASTP 181
QY 182 TAALAVIRHVGKRYRFLVSVISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFAA 241
Db 182 TADLSVISYTPGKRYRFLVSVISCDPNYTFSDGHNMTIETDSINTAPLVVDSIQIFAA 241
QY 242 QRYSEVLNANOTVGNVYVRANPNFTGTVGAGGINSAILRYQGPVAPETTTTTSVIPLI 301
Db 242 QRYSEVLNANQAVDNVIRANPNFTGTVGAGGINSAILRYDGAAPETTTTTSVAPLN 301
QY 302 ETNLHPLARMVPGSTPGGVGDKALNLAFAFNFTGTFINNAFTPTPTVPLVLIISGAQT 361
Db 302 EVNLHPLVATVPGSPVAGGVDLAINMAFNFTGTFINNAFTPTPTVPLVLIISGAQN 361
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNDPI 421
Db 362 AQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPHLLGHAFVAVRSAGSTTYNDPI 421
QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDFHLDAFAIYFAEDVADVKAANPVP 481
Db 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDFHLDAFAIYFAEDVADVKAANPVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDALDPSDQ 499

Search completed: December 14, 2002, 08:25:24
Job time : 74 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 07:47:02 ; Search time 84 Seconds
(without alignments)
1224.018 Million cell updates/sec

Title: US-09-786-960-2
Perfect score: 2669
Sequence: 1 AIGPVASIVVANAFVSPDGF.....VPKAWSDLCPIYDGLSEANQ 499

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_todent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2599	97.4	519	3 Q96UK8	Q96UK8 trаметes ve
2	2343.5	87.8	519	3 Q13420	Q13420 basidiomyce
3	2195	82.2	520	3 Q96UT7	Q96UT7 trаметes ve
4	2194	82.2	520	3 Q13448	Q13448 coriolus ve
5	2194	82.2	520	3 Q8TG94	Q8TG94 trаметes pu
6	2187	81.9	520	3 Q8TFM1	Q8TFM1 trаметes ve
7	2186	81.9	520	3 Q13421	Q13421 basidiomyce
8	2176	81.5	520	3 Q94222	Q94222 trаметes ve
9	2145	80.4	518	3 Q96TR6	Q96TR6 pycnopus
10	2143	80.3	518	3 Q96VA5	Q96VA5 pycnopus
11	2140	80.2	518	3 Q59896	Q59896 pycnopus
12	2138	80.1	518	3 Q9UVQ2	Q9UVQ2 pycnopus
13	2137	80.1	524	3 Q13422	Q13422 basidiomyce
14	2125	79.6	518	3 Q9HDS9	Q9HDS9 polyporus c
15	2107.5	79.0	521	5 Q61263	Q61263 trachyderma
16	2102.5	78.8	521	3 Q9UVU8	Q9UVU8 pycnopus

Q9UVQ5 marasmius q
Q12571 basidiomyce
Q9Hdq0 trаметes tr
Q8tg93 trаметes pu
Q13456 coriolus ve
Q8tl8 coriolus hi
Q9Hds8 polyporus c
Q9Hds7 polyporus c
Q59944 ceriporiops
Q8wz93 lentinula e
Q9uvy4 pleurotus o
Q9p84 coriolopsis
Q9y781 coprinus ci
Q9hg17 ganoderma l
Q9y782 coprinus ci
Q60199 pleurotus o
Q74171 schizophyll
Q8xiw3 lentinula e
Q8wz10 lentinula e
Q9vt6 lentinula e
Q9y780 coprinus ci
Q9vt5 lentinula e
Q9hft4 pleurotus s
Q8wzh9 lentinula e
Q8xiw2 lentinula e
Q96tr4 pleurotus o
Q9p8b9 coprinus co
Q9uv01 heterobasid
Q9uu5 heterobasid

17 2029.5 76.0 517 3 Q9UVQ5
18 2026.5 75.9 517 3 Q12571
19 2016.5 75.6 517 3 Q9HDQ0
20 1927.5 72.2 526 3 Q8TG93
21 1915 71.7 526 3 Q13456
22 1893 70.9 518 3 Q8TFL8
23 1873 70.2 524 3 Q9HDS8
24 1806.5 67.7 477 3 Q9HDS7
25 1800 67.4 520 3 Q59944
26 1772 66.4 518 3 Q8WZG3
27 1739.5 65.2 533 3 Q9UVY4
28 1723 64.6 517 3 Q9P84
29 1704.5 63.9 517 3 Q9Y781
30 1677 62.8 388 3 Q9HG17
31 1667.5 62.5 516 3 Q9Y782
32 1629 61.0 533 3 Q60199
33 1598 59.9 518 3 Q74171
34 1578.5 59.1 533 3 Q8XIW3
35 1577.5 59.1 533 3 Q8WZIO
36 1538 57.6 526 3 Q9UVT6
37 1533 57.4 539 3 Q9Y780
38 1523 57.1 526 3 Q9UVT5
39 1490.5 55.8 465 3 Q9HFT4
40 1475.5 55.3 505 3 Q8WZH9
41 1431.5 53.6 548 3 Q8XIW2
42 1222 45.8 521 3 Q96TR4
43 986.5 37.0 362 3 Q9P8B9
44 949.5 35.6 329 3 Q9UV01
45 943.5 35.4 329 3 Q9UU5

ALIGNMENTS

RESULT 1

Q96UK8 PRELIMINARY; PRT; 519 AA.
ID Q96UK8;
AC Q96UK8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Laccase 1 (EC 1.10.3.2).
GN LAC1.
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CUI;
RA McClean K.H., O'Brien M.M., Dobson A.D.W.;
RT "Trametes versicolor laccase (lac1) mRNA sequence.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY049725; AAL00887.1; -;
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 519 AA; 55998 MW; 8C9C6934DEAE3E0A CRC64;

Query Match 97.4%; Score 2599; DB 3; Length 519;
Best Local Similarity 97.4%; Pred. No. 2.9e-177;
Matches 486; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 AIGPVASIVVANAFVSPDGF...Q96UK8 60
Db 21 AIGPVASIVVANAFVSPDGF...Q96UK8 80
QY 61 TSIHHGFFQAGTNWADGPAFVNOCPIASGHGFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 81 TSIHHGFFQAGTNWADGPAFVNOCPIASGHGFLYDFHVPDQAGTFWYHSHLSTQYCDGL 140
QY 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLINGLRASST 180

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|||||
141 RGFVYDVKPDHASYDYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 200
Db

181 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
QY |||||
201 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 260
Db

241 AQRYSFVLNANOTVGNWYWRANPNFGTVGAGGINSAILRYOGAPVAEPTTTOTTTSVPL 300
QY |||||
261 AQRYSFVLNANOTVGNWYWRANPNFGTVGAGGINSAILRYOGAPVAEPTTTOTTTSVPL 320
Db

301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTVPVLLQILSGAQ 360
QY |||||
321 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTVPVLLQILSGAQ 380
Db

361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGSTTYNYNDP 420
QY |||||
381 TAQELLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGSTTYNYNDP 440
Db

421 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
QY |||||
441 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLEAGFAIYFAEDVADVKAANPV 500
Db

481 PKAWSDLCPYDGLSEANQ 499
QY |||||
501 PKAWSDLCPYDGLSEADQ 519
Db

RESULT 2
O13420 PRELIMINARY; PRT; 519 AA.
ID O13420
AC O13420;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phenoloxidase (EC 1.10.3.2).
GN POX1.
OS basidiomycete CECT 20197.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae.
OX NCBI_TaxID=51095;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT N.197;
RX MEDLINE=97355933; PubMed=9212414;
RA Mansur M., Suarez T., Fernandez-Larrea J.B., Brizuela M.A.,
RA Gonzalez A.E.;
RT "Identification of a laccase gene family in the new lignin-degrading
RT basidiomycete CECT 20197."
RL Appl. Environ. Microbiol. 63:2637-2646(1997).
DR EMBL; U65399; AAB63443.1; -
DR HSSP; P37064; IAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 519 AA; 55665 MW; CD226C498770DDE4 CRC64;

Query Match 87.8%; Score 2343.5; DB 3; Length 519;
Best Local Similarity 86.5%; Pred. No. 4.8e-159;
Matches 431; Conservative 25; Mismatches 41; Indels 1; Gaps 1;

QY 1 AIGPVASLVANAPVSPDGLRDALVINGVVPSPPLITGKGRFQNLNVVDLTNHSMLKS 60
Db |||||
22 AVGE-ADLTITNAVYAPGDSRDAVVVGVFPGLITGKGRFQNLNVVDLTNHSMLKS 80
Db |||||
61 TSIHHGFFOAGTNNWADGPAFVNCQPIASGHSFLYDFHVPDQAGFWYHSHLSTQYCDGL 120
QY |||||
81 TSIHHGFFOAGTNNWADGPAFVNCQPIASGHSFLYDFHVPDQAGFWYHSHLSTQYCDGL 140
Db |||||
121 RGFVYDVKPDHASYDYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 180
QY |||||
141 RGFVYDVKPDHASYDYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 200
Db |||||
```

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181 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
QY |||||
201 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFA 260
Db |||||
241 AQRYSFVLNANOTVGNWYWRANPNFGTVGAGGINSAILRYOGAPVAEPTTTOTTTSVPL 300
QY |||||
261 AQRYSFVLNANOTVGNWYWRANPNFGTVGAGGINSAILRYOGAPVAEPTTTOTTTSVPL 320
Db |||||
301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTVPVLLQILSGAQ 360
QY |||||
321 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTVPVLLQILSGAS 380
Db |||||
361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGSTTYNYNDP 420
QY |||||
381 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGSTTYNYNDP 440
Db |||||
421 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
QY |||||
441 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLEAGFAIYFAEDVADVKAANPV 500
Db |||||
481 PKAWSDLCPYDGLSEAN 498
QY |||||
501 PKAWSDLCPYDALAEGD 518
Db |||||

RESULT 3
O96UT7 PRELIMINARY; PRT; 520 AA.
ID O96UT7
AC Q96UT7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Laccase B precursor (BC 1.10.3.2).
GN LAC1.
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 32745;
RA Jolivaldt C., Madzak C., Caminade E., Mouglin C.;
RT "2,5-xylidine induced laccase from the basidiomycete Trametes
RT versicolor ATCC 32745."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414109; AAL07440.1; -
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Oxidoreductase; Signal.
FT SIGNAL
SQ SEQUENCE 520 AA; 55576 MW; F3241CB929C247F9 CRC64;

Query Match 82.2%; Score 2195; DB 3; Length 520;
Best Local Similarity 79.9%; Pred. No. 1.9e-148;
Matches 398; Conservative 35; Mismatches 65; Indels 0; Gaps 0;

QY 2 IGPVASLVANAPVSPDGLRDALVINGVVPSPPLITGKGRFQNLNVVDLTNHSMLKST 61
Db |||||
23 IGPVADLTITNAVYAPDGSFQAVVGVFPGLITGKGRFQNLNVVDLTNHSMLKST 82
Db |||||
62 SIHHGFFOAGTNNWADGPAFVNCQPIASGHSFLYDFHVPDQAGFWYHSHLSTQYCDGLR 121
QY |||||
83 SIHHGFFOAGTNNWADGPAFVNCQPIASGHSFLYDFQVDPQAGFWYHSHLSTQYCDGLR 142
Db |||||
122 GPFVYDVKPDHASYDYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 181
QY |||||
143 GPFVYDNDPAADLYDVNDNDTITLVDWYHVAAKLPAFPLGADATVINGLGRSPSTT 202
Db |||||
182 TAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIQIFAA 241
QY |||||
203 TADLSVISTPCKRYRFRFLVSLSCDPNTFTSIDGHNMTIITDSTINTAPLVVDSIQIFAA 262
Db |||||
```



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QY 242 QRYSFVLNANQTYGNTVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSTVIPLI 301
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 QRYSFVLEAQAQVNDWIRANPNFGVGTGGINSAILRYDGAANVEPTTTQTTSTAPLN 322
QY 302 ETNLHPLARMPVPGSPGVDKALNLAFAFNNGTNNFNNATFTPTTPVVLQLIISGAQT 361
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 EVNLHPLVATAVPGSPVAGVDLAINMAFNENGTNFFINGASFTPTTPVVLQLIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNDPI 421
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 AQDLLSGSVYSLPSNADIEISFPATAAAGAPHPFLHGHAFVAVRSAGSTTYNDNPI 442
QY 422 FROWSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADYKAANPVP 481
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 FROWSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDIPDVASANPVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
: ||| ||| ||| : |||
Db 503 QAWSDLCPYDARDPSDQ 520

RESULT 4
Q13448
ID Q13448 PRELIMINARY; PRT; 520 AA.
AC Q13448;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN CVL3.
OS Coriolus versicolor.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriolus.
OX NCBI_TaxID=57466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Mikuni J.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Iimura Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; D13372; BAA22153.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase; Signal.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 520 AA; 55528 MW; F9429BEAC9D71B0 CRC64;

Query Match 82.2%; Score 2194; DB 3; Length 520;
Best Local Similarity 79.9%; Pred. No. 2.2e-148;
Matches 398; Conservative 35; Mismatches 65; Indels 0; Gaps 0;

QY 2 IGVPASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKST 61
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 IGVPADLTITNAAVSPDGSRAQVAVNGGTPGLITGNMGDRFQNLNVVDLTNHSMLKST 82
QY 62 SIHWHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 121
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 SIHWHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 142
QY 122 GPFWVYDPPKDPHASRYDNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLRASSTP 181
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GPFWYDPPNDPADLDVDNDQTVITLVDMYHVAANKLGPAPPLGADATLNGLRASSTP 202
QY 182 TAALAVINVOHGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 241
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TADLSVISVTPGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 262
QY 122 GPFWVYDPPKDPHASRYDNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLRASSTP 181
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GPFWYDPPNDPADLDVDNDQTVITLVDMYHVAANKLGPAPPLGADATLNGLRASSTP 202
QY 182 TAALAVINVOHGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 241
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TADLSVISVTPGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 262
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QY 242 QRYSFVLNANQTYGNTVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSTVIPLI 301
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 QRYSFVLEAQAQVNDWIRANPNFGVGTGGINSAILRYDGAANVEPTTTQTTSTAPLN 322
QY 302 ETNLHPLARMPVPGSPGVDKALNLAFAFNNGTNNFNNATFTPTTPVVLQLIISGAQT 361
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 EVNLHPLVATAVPGSPVAGVDLAINMAFNENGTNFFINGASFTPTTPVVLQLIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNDPI 421
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 AQDLLSGSVYSLPSNADIEISFPATAAAGAPHPFLHGHAFVAVRSAGSTTYNDNPI 442
QY 422 FROWSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADYKAANPVP 481
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 FROWSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDIPDVASANPVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
: ||| ||| ||| : |||
Db 503 QAWSDLCPYDALDPSDQ 520

RESULT 5
Q8TG94
ID Q8TG94 PRELIMINARY; PRT; 520 AA.
AC Q8TG94;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Laccase 2 (EC 1.10.3.2).
GN LAP2.
OS Trametes pubescens.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=154538;
RN [1]
RP SEQUENCE FROM N.A.
RA Galhaup C., Goller S.P., Peterbauer C.K., Strauss J., Haltrich D.;
RT "Purification, Characterization, Cloning, and Expression of the
RT Predominant Laccase from Trametes pubescens.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414807; AAM18407.1; -.
KW Oxidoreductase.
SQ SEQUENCE 520 AA; 55519 MW; CAAA35032FAE2524 CRC64;

Query Match 82.2%; Score 2194; DB 3; Length 520;
Best Local Similarity 79.9%; Pred. No. 2.2e-148;
Matches 398; Conservative 37; Mismatches 63; Indels 0; Gaps 0;

QY 2 IGVPASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKST 61
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 IGVPADLTITNAAVSPDGSRAQVAVNGGTPGLITGNMGDRFQNLNVVDLTNHSMLKST 82
QY 62 SIHWHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 121
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 SIHWHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 142
QY 122 GPFWVYDPPKDPHASRYDNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLRASSTP 181
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GPFWYDPPNDPADLDVDNDQTVITLVDMYHVAANKLGPAPPLGADATLNGLRASSTP 202
QY 182 TAALAVINVOHGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 241
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TADLSVISVTPGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 262
QY 242 QRYSFVLNANQTYGNTVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSTVIPLI 301
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 QRYSFVLEAQAQVNDWIRANPNFGVGTGGINSAILRYDGAANVEPTTTQTTSTAPLN 322
QY 302 ETNLHPLARMPVPGSPGVDKALNLAFAFNNGTNNFNNATFTPTTPVVLQLIISGAQT 361
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 EVNLHPLVATAVPGSPVAGVDLAINMAFNENGTNFFINGASFTPTTPVVLQLIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNDPI 421
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RESULT 8
O94222
ID O94222 PRELIMINARY; PRT; 520 AA.
AC O94222;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN LCC2.
OS Trameetes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trameetes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SBUG1050;
RA Jonsson L., Nyman P.O.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18012; CAA77015.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase; Signal.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 520 LACCASE.
SQ SEQUENCE 520 AA; 55489 MW; 560984A5DF2A7D6B CRC64;

Query Match 81.5%; Score 2176; DB 3; Length 520;
Best Local Similarity 79.3%; Pred. No. 4.2e-147;
Matches 395; Conservative 37; Mismatches 66; Indels 0; Gaps 0;

QY 2 IGPVASLVANAPVSPDGLRDAIVVNGVSPDLITGKGRFQNLNVVDITLTHNSMLKST 61
DB 1 IGPVADLTITNAAVSPDGSFQAVVNGTGPCLITGNKGRFQNLNVIDLTHMLKST 82
QY 62 SIHWGFFQAGTNWADGPAFVNOCPDASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
DB 83 SIHWGFFQAGTNWADGPAFVNOCPDASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGLR 142
QY 122 GPFVYDPKPHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLINGLRSASTP 181
DB 143 GPFVYDNDPAADLYDVNDNDTITLADWYHVAAKLGPAPLGLADATLINGLRSPTT 202
QY 182 TAALAVINVOHGKRYRFRFLYSISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFAA 241
DB 203 TADLTVISVTPGKRYRFRFLYSISCDPNHTFSIDGHNMTHIETDSTINAPLVVDSIQIFAA 262
QY 242 QRYSPVLNANTGVNMYVRANPFGTVGFAGGINSAILRYOGAPVAEPTTTQTTTSVPLI 301
DB 263 QRYSPVLNANTGVNMYVRANPFGTVGFAGGINSAILRYOGAPVAEPTTTQTTTSVPLI 322
QY 302 ETNLHPLARMVPVPGSPTPGGVDKALNLFNFNGTFFINNATFTPTPVLLQILSGAQT 361
DB 323 EVNLHPLVATAPVPGSPAGGVDLAINMAFNENGTFINGASFTPTPVLLQILSGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIETLTPALAPGAPHPFLHGHAFVAVRSAGSTTYNDPI 421
DB 383 AQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPFLHGHAFVAVRSAGSTTYNDPI 442
QY 422 FRDVTSTGTPAAGDNVTIRFOTDNPFWFLCHIDFHLDAAGFAIVFAEDVADYKAANVP 481
DB 443 FRDVTSTGTPAAGDNVTIRFOTDNPFWFLCHIDFHLDAAGFAIVFAEDVADYKAANVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
DB 503 QAWSDLCPYDARDPSDQ 520

RESULT 9
Q96TR6
ID Q96TR6 PRELIMINARY; PRT; 518 AA.
AC Q96TR6;
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DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Laccase precursor.
GN LCC1.
OS Pycnopus coccineus (Orange bracket).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Pycnopus.
OX NCBI_TaxID=158605;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoshida H., Nakao M., Kubo K., Hakukawa T., Morimasa K., Akada R.,
RA Nishizawa Y.;
RL "Isolation of Five Laccase Gene Sequences from the White-Rot Fungus
Trameetes sanguinea by PCR, and Cloning, Characterization and
Expression of the Laccase cDNA in Yeasts.";
RL J. Biosci. Bioeng. 0:0-0(2001).
DR EMBL; AB072703; BAB69775.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
SQ SEQUENCE 518 AA; 55877 MW; 64950AACA3A28F47 CRC64;

Query Match 80.4%; Score 2146; DB 3; Length 518;
Best Local Similarity 78.3%; Pred. No. 5.8e-145;
Matches 390; Conservative 40; Mismatches 66; Indels 2; Gaps 1;

QY 1 AIGPVASLVANAPVSPDGLRDAIVVNGVSPDLITGKGRFQNLNVVDITLTHNSMLKS 60
DB 22 AIGPVADLTITNAAVSPDGSFQAVVNGTGPCLITGNKGRFQNLNVIDLTHMLKST 81
QY 61 TSIHWGFFQAGTNWADGPAFVNOCPDASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 82 TSIHWGFFQAGTNWADGPAFVNOCPDASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 141
QY 121 RGFVYDYPKPHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLINGLRSAST 180
DB 142 RGFVYDNDPAADLYDVNDNDTITLADWYHVAAKLGPAPLGLADATLINGLRSPTT 201
QY 181 PTAALAVINVOHGKRYRFRFLYSISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFA 240
DB 202 TAADLTAVISVTPGKRYRFRFLYSISCDPNHTFSIDGHNMTHIETDSTINAPLVVDSIQIFA 261
QY 241 AORYSPVLNANTGVNMYVRANPFGTVGFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 300
DB 262 AQRYSPVLNANTGVNMYVRANPFGTVGFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 321
QY 301 IETNLHPLARMVPVPGSPTPGGVDKALNLFNFNGTFFINNATFTPTPVLLQILSGAQ 360
DB 322 NEVDLHPLTMAVPCRPPEPGVDTPLNMYVFNFGTFFINDHSFVPPSPVLLQILSGAQ 381
QY 361 TAQDLLPAGSVYPLPAHSTIETLTPALAPGAPHPFLHGHAFVAVRSAGSTTYNDP 420
DB 382 AQDLLPAGSVYPLPSNSSIEISFPATANAPGAPHPFLHGHAFVAVRSAGSTTYNDP 441
QY 421 IFRDVTSTGTPAAGDNVTIRFOTDNPFWFLCHIDFHLDAAGFAIVFAEDVADYKAANVP 480
DB 442 IFRDVTSTGTP--GDNVTIRFOTDNPFWFLCHIDFHLDAAGFAIVFAEDVADYKAANVP 499
QY 481 PKAWSDLCPYDGLSEAN 498
DB 500 PQWSNDCLPYDALDPSD 517

RESULT 10
Q96VA5
ID Q96VA5 PRELIMINARY; PRT; 518 AA.
AC Q96VA5;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
```


QY 61 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTOYCDGL 120
 Db 82 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTOYCDGL 141
 QY 121 RGFVYVDPKDHASRYDVNDNESTVITLTDWYHVAALGPRPLGADATLNGLSRST 180
 Db 142 RGFVYVDPKDHASRYDVNDNESTVITLTDWYHVAALGPRPLGADATLNGLSRST 201
 QY 181 PTAALAVINQHGKRYRFRFLVSTISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFA 240
 Db 202 TTAALAVINQHGKRYRFRFLVSTISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFA 261
 QY 241 AQRYSVLNANTGVNWRANPFGTGVFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 300
 Db 262 AQRYSVLNANTGVNWRANPFGTGVFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 321
 QY 301 IETNLHPLARMVPVPGSPTGGVDKALNLAFFNGTFFNNATFTPTTPVLLQILSGAQ 360
 Db 322 IETNLHPLARMVPVPGSPTGGVDKALNLAFFNGTFFNNATFTPTTPVLLQILSGAQ 381
 QY 361 TAQDLLPAGSVYPLPAHSTIETLPATALAPGAPHPFHLGHAFVVRSGASTTYNDP 420
 Db 382 AAQDLVPGSVYPLPSNSSIEISFPATANAPGTPHPFHLGHAFVVRSGASTTYNDP 441
 QY 421 IFRDVYSTGTGAAGDNTTFRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 480
 Db 442 IFRDVYSTGTGAAGDNTTFRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 499
 QY 481 PRAWSDLCPIYDGLSEAN 498
 Db 500 PRAWSDLCPIYDGLSEAN 517

RESULT 12

Q9UVQ2 ID Q9UVQ2 PRELIMINARY; PRT; 518 AA.
 AC Q9UVQ2
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Laccase (EC 1.10.3.2).
 GN LAC1.
 OS Pycnopus cinnabarinus
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllum; Pycnopus.
 OX NCBI_TaxID=5643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-I-937;
 RA Moukha S., Otterbein L., Record E.;
 RT "Cloning, characterization and expression of the gene encoding an
 extracellular laccase from Pycnopus cinnabarinus I-937 strain; an
 allele showing a great divergence at the nucleic acid level with the
 Lcc 3-1 gene of Strain ATCC 200478.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-I-937;
 RA Otterbein L., Record E., Moukha S.;
 RT "Cloning of a cDNA encoding laccase protein from Pycnopus
 cinnabarinus I-937.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF170093; AAF13052.1;
 DR EMBL: AF152170; AAG13724.1;
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 518 AA; 56292 MW; 329714CF463ED081 CRC64;

Query Match 80.1%; Score 2138; DB 3; Length 518;
 Best Local Similarity 77.7%; Pred. NO. 2.2e-144;
 Matches 387; Conservative 44; Mismatches 65; Indels 2; Gaps 1;

QY 1 AIGPVAELVYVAPSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNHSMLKS 60
 Db 22 AIGPVAELVYVAPSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNHSMLKS 81
 QY 61 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTOYCDGL 120
 Db 82 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTOYCDGL 141
 QY 121 RGFVYVDPKDHASRYDVNDNESTVITLTDWYHVAALGPRPLGADATLNGLSRST 180
 Db 142 RGFVYVDPKDHASRYDVNDNESTVITLTDWYHVAALGPRPLGADATLNGLSRST 201
 QY 181 PTAALAVINQHGKRYRFRFLVSTISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFA 240
 Db 202 TTAALAVINQHGKRYRFRFLVSTISCDPNYTFSDGHNLTVIEVDGINSOPLLVDSIQIFA 261
 QY 241 AQRYSVLNANTGVNWRANPFGTGVFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 300
 Db 262 AQRYSVLNANTGVNWRANPFGTGVFAGGINSAILRYOGAPVAEPTTTQTTTSVPL 321
 QY 301 IETNLHPLARMVPVPGSPTGGVDKALNLAFFNGTFFNNATFTPTTPVLLQILSGAQ 360
 Db 322 IETNLHPLARMVPVPGSPTGGVDKALNLAFFNGTFFNNATFTPTTPVLLQILSGAQ 381
 QY 361 TAQDLLPAGSVYPLPAHSTIETLPATALAPGAPHPFHLGHAFVVRSGASTTYNDP 420
 Db 382 AAQDLVPGSVYPLPSNSSIEISFPATANAPGTPHPFHLGHAFVVRSGASTTYNDP 441
 QY 421 IFRDVYSTGTGAAGDNTTFRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 480
 Db 442 IFRDVYSTGTGAAGDNTTFRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 499
 QY 481 PRAWSDLCPIYDGLSEAN 498
 Db 500 PRAWSDLCPIYDGLSEAN 517

RESULT 13

OL3422 ID OL3422 PRELIMINARY; PRT; 524 AA.
 AC OL3422
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Phenoloxidase (EC 1.10.3.2).
 GN POX3.
 OS basidiomycete CECT 20197.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Polyporaceae.
 OX NCBI_TaxID=51095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CECT 20197;
 EX MEDLINE=97355933; PubMed=9212414;
 RA Mansur M., Suarez T., Fernandez-Larrea J.B., Brizuela M.A.,
 RT "Identification of a laccase gene family in the new lignin-degrading
 basidiomycete CECT 20197.";
 RL Appl. Environ. Microbiol. 63:2637-2646(1997).
 DR EMBL: U55401; AAB63445.1;
 DR HSSP: P37064; IAOZ.
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 524 AA; 56240 MW; 490BFA4AB1168608 CRC64;

Query Match 80.1%; Score 2137; DB 3; Length 524;
 Best Local Similarity 77.8%; Pred. NO. 2.6e-144;
 Matches 388; Conservative 39; Mismatches 72; Indels 0; Gaps 0;
 QY 1 AIGPVAELVYVAPSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNHSMLKS 60

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Db 26 AVGVTDLTISNANVSDGQRAAVVANGVGPGLINGOKGDFHQINNVNQLNHHMLKS 85
QY 61 TSIHWHGFFQAGTNWADGPAFVNCPIASGHSFLYDFHPDQAGTFWYHSHLSSTQYCDGL 120
Db 86 TSIHWHGFFQKGTNWADGPAFVNCPIATGHSFLYDFHPDQAGTFWYHSHLSSTQYCDGL 145
QY 121 RGPFWYDQKDPHASRYDVNDNESTVITLTDWYHTAARLGRPRPLGADATLNGLSAST 180
Db 146 RGPFWYDQKDPHASRYDVNDNESTVITLTDWYHTAARLGRPRPRADATLNGLSRSTDT 205
QY 181 PTAALAVINVOHGKRYRFRFLVSLVSCDPNTFTSIDGHNLTAVIEVDGINSQPLLVDLSIQIFA 240
Db 206 PTADLAVIKVTSGRKRYRFRFLVSLVSCDPNTFTSIDGHNLTAVIEVDGINSQPLLVDLSIQIFA 265
QY 241 AQRYSFVLNANQTYGVNWRANPNFTGTFAGGINSAILRYQAGAPVAEPTTTQTTSTVPL 300
Db 266 GORYSFVLEANOAVDNYWVRANPNFTGTFAGGINSAILRYQAGAPVAEPTTTQTTSTKPL 325
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGTNEFFINNATFTPTVPVLLQLLSGA 360
Db 326 AETDLVPLASMPVPGSPVSGVDKALNLAFFNGTNEFFINNATFTPTVPVLLQLLSGA 385
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFLHGHAFVAVRSAGSTTYNNDP 420
Db 386 DASALLPSGDVYVSPSNATIELTPTATGAPGAPHPFLHGHAFVAVRSAGSTTYNNDP 445
QY 421 IFRDVVSTGTGAAGDNVTIRFQTDNPGPWFHCHIDHLDAGFAIVFAEDVADVKAANPV 480
Db 446 IWRDVVSTGTGAAGDNVTIRFQTDNPGPWFHCHIDHLDAGFAIVFAEDVADVKAANPV 505
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 506 PQAWSDLCPYDAUDPSDQ 524

RESULT 14
Q9HDS9 PRELIMINARY; PRT; 518 AA.
AC Q9HDS9;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Laccase LCC3-1 (EC 1.10.3.1).
GN LCC3-1.
OS Polyporus ciliatus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae; Polyporus.
OX NCBI_TaxID=134555;
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RP SEQUENCE FROM N.A.
RC STRAIN=TH1; TISSUE=VEGETATIVE MYCELIA;
RA Schnee C., Eggert C.;
RT "Isolation and characterization of three laccase genes from the white-
rot fungus Polyporus ciliatus and their expression during fruiting.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF176230; AAG09229.1; -
DR HSP; P37064; IAOZ
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 518 AA; 55792 MW; 6494CA7C3FD0B29F CRC64;

Query Match 79.6%; Score 2125; DB 3; Length 518;
Best Local Similarity 78.0%; Pred. No. 1.8e-143;
Matches 390; Conservative 47; Mismatches 59; Indels 4; Gaps 3;

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Db 321 LLETDLHPFTPTVPVPGNPTGGADFNLAFFNGTDFSIINGATFTFPSPVPLQLLSGA 380
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Db 381 NSAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFLHGHAFVAVRSAGSTTYNND 440
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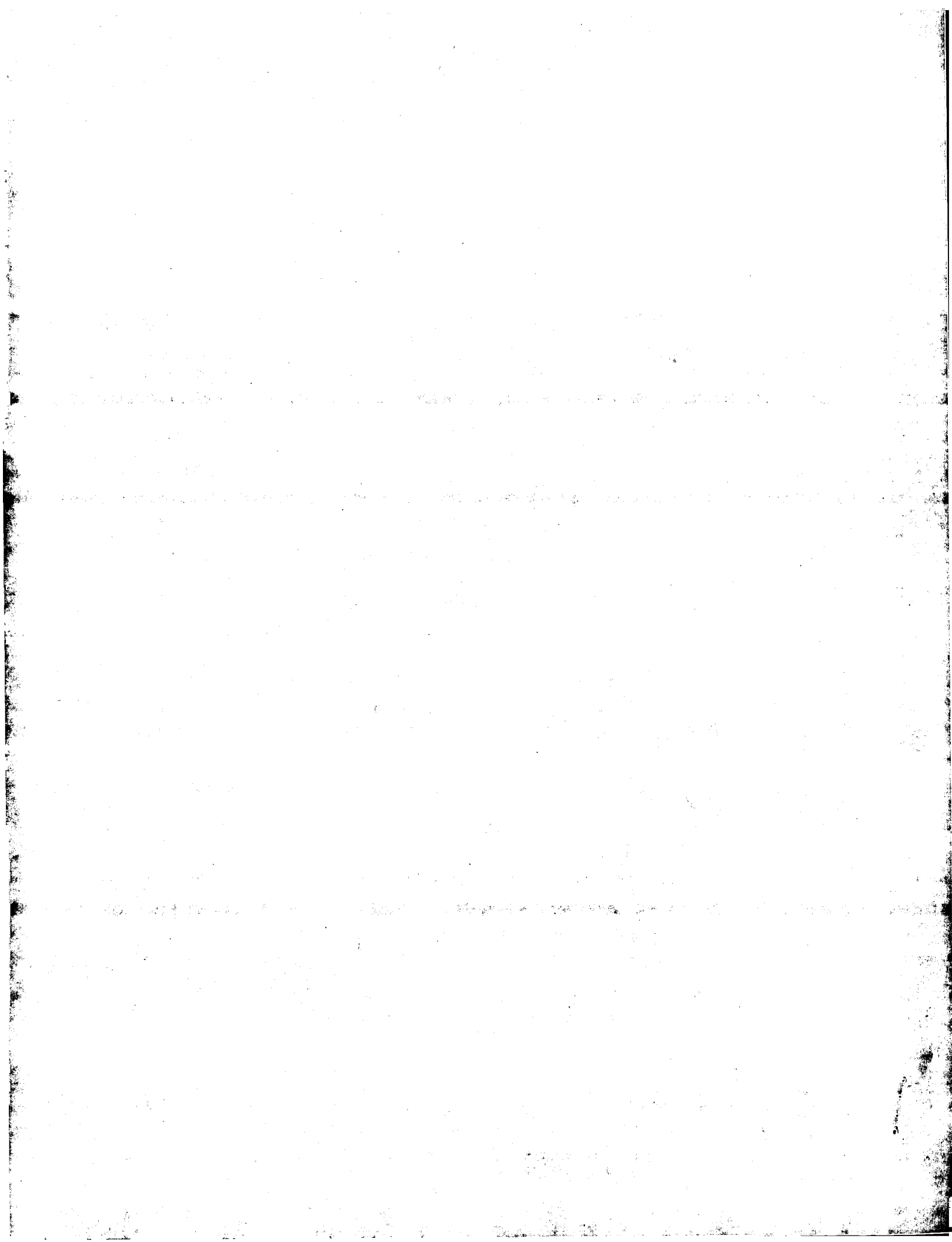
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DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Bilirubin oxidase precursor.
OS Trachyderma tsunodae.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Trachyderma.
OX NCBI_TaxID=65050;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-2593;
RA Iwamoto H., Watanabe H., Minakami M., Hirose J., Hiromi K., Mukai H.,
RA Yoshioka H., Kato I.;
RT "Purification, Characterization, and Molecular Cloning of Bilirubin
Oxidase from Trachyderma tsunodae K-2593.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB006824; BAA28668.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 521 AA; 56456 MW; ED078214DD2986D4 CRC64;

Query Match 79.0%; Score 2107.5; DB 5; Length 521;
Best Local Similarity 77.0%; Pred. No. 3.3e-142;
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Search completed: December 14, 2002, 08:27:58
Job time : 89 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 08:25:32 ; Search time 27 seconds
(without alignments)
543.779 Million cell updates/sec

Title: US-09-786-960-2
Perfect score: 2669
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2656	99.5	499	4	US-09-399-886-3
4	2656	99.5	499	4	US-09-396-280-3
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6	2656	99.5	519	1	US-08-462-484-4
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22	1842	69.0	511	5	PCT-US95-07536-8
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31 1716 64.3 548 4 US-09-576-281-4 Sequence 4, Appli
32 1704.5 63.9 517 3 US-08-689-421-33 Sequence 33, Appl
33 1704.5 63.9 517 4 US-09-389-528-33 Sequence 33, Appl
34 1704.5 63.9 517 4 US-09-181-827A-33 Sequence 33, Appl
35 1667.5 62.5 516 3 US-08-689-421-29 Sequence 29, Appl
36 1667.5 62.5 516 4 US-09-389-528-29 Sequence 29, Appl
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45 1533 57.4 539 4 US-09-576-281-1 Sequence 1, Appli

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ALIGNMENTS

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RESULT 1
US-09-032-315-3
; Sequence 3, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-032-315-3

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Query Match 99.5%; Score 2656; DB 2; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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RESULT 2
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; Sequence 3, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59983530 No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,318A
; FILING DATE: December 18, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-993-318A-3
Query Match 99.5%; Score 2656; DB 2; Length 499;
Best Local Similarity 99.4%; Pred. No. 7-7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3
US-09-399-886-3
; Sequence 3, Application US/09399886
; Patent No. 6140092
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6140092o No. 6140092disk of No. 6140092th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,886
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318


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; Sequence 3, Application US/09576281
; Patent No. 6277611
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6277611o No. 6277611disk of No. 6277611th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/576,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-576-281-3

Query Match          99.5%; Score 2656; DB 4; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 301 IETNLHPLARMPVPGSPGCGVDKALNLAENFNCTNFFINNATFTPTVPVLLQLISGAQ 360

; Sequence 4, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboege, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Asalyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-484-4

Query Match          99.5%; Score 2656; DB 1; Length 519;
Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGFRLDAIVVGVVPSPLITGKGRFQLNVVDTLNHSMLKS 60
Db 21 AIGPVASLVVANAPVSPDGFRLDAIVVGVVPSPLITGKGRFQLNVVDTLNHSMLKS 80
QY 61 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 81 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 140
QY 121 RGPVVYDVKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 180
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Db 141 RGFVVYDPKDPHASKRYDNDNESTVITLTDWYHTAARLGPKEPLGADATLNGLSAST 200
QY 181 PTAALAVINVQHGKRYRRLVLSISCDPNYTFSIDGHNLTVEVDGINSOPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRRLVLSISCDPNYTFSIDGHNLTVEVDGINSOPLLVDSIQIFA 260
QY 241 AQRYSEVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
Db 261 AQRYSEVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 380
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 440
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 7
US-08-441-147-4
; Sequence 4, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Paule
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441.147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-147-4
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Query Match 99.5%; Score 2656; DB 1; Length 519;

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Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0:

QY 1 AIGPVASIVVANAPVSPDGFLDAIVVAGVVPSPITLTKGKDRFQLVNVYDTLTNHSMLKS 60
Db 21 AIGPVASIVVANAPVSPDGFLDAIVVAGVVPSPITLTKGKDRFQLVNVYDTLTNHSMLKS 80
QY 61 TSIHHGTFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTFWYHSHLSTOYCDGL 120
Db 81 TSIHHGTFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTFWYHSHLSTOYCDGL 140
QY 121 RGFVVYDPKDPHASKRYDNDNESTVITLTDWYHTAARLGPKEPLGADATLNGLSAST 180
Db 141 RGFVVYDPKDPHASKRYDNDNESTVITLTDWYHTAARLGPKEPLGADATLNGLSAST 200
QY 181 PTAALAVINVQHGKRYRRLVLSISCDPNYTFSIDGHNLTVEVDGINSOPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRRLVLSISCDPNYTFSIDGHNLTVEVDGINSOPLLVDSIQIFA 260
QY 241 AQRYSEVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
Db 261 AQRYSEVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 380
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 440
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 8
PCT-US95-07536-4
; Sequence 4, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:
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SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07536-4

Query Match 99.5%; Score 2656; DB 5; Length 519;
Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKGGDRFQLNVVDLTNHSMLKS 60
DB 21 AIGPVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKGGDRFQLNVVDLTNHSMLKS 80
QY 61 TSIHHGFFQAGNWDGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 81 TSIHHGFFQAGNWDGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 140
QY 121 RGPVVYDPRDPRHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 180
DB 141 RGPVVYDPRDPRHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 200
QY 181 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTVIEVDGINSQPLLVDLSIQIFA 240
DB 201 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTVIEVDGINSQPLLVDLSIQIFA 260
QY 241 AQRYSFVLNANOTVGNVWVRANPNFVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 300
DB 261 AQRYSFVLNANOTVGNVWVRANPNFVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 320
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLFNFGTNNFNNATFTPTPVVLLQILSGAQ 360
DB 321 IETNLHPLARMPVPGSPPTGGVDKALNLFNFGTNNFNNATFTPTPVVLLQILSGAQ 380
QY 361 TAQDLLPAGSVYPLPAHSTIETLTPATAPAGAPHPHHLGHAFVAVRSAGSTTYNNDP 420
DB 381 TAQDLLPAGSVYPLPAHSTIETLTPATAPAGAPHPHHLGHAFVAVRSAGSTTYNNDP 440
QY 421 IFRDVSSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
DB 441 IFRDVSSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 501 PKAWSDLCPYDGLSEANQ 519

RESULT 9
US-09-032-315-2

; Sequence 2, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5985818 of No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-032-315-2

Query Match 82.5%; Score 2201; DB 2; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;

QY 2 IGPVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKGGDRFQLNVVDLTNHSMLKST 61
DB 2 IGPVADLTITNAVSPDGSFQAVVNGVGTPLITGNGMDRFLQNLVDLTNHTMLKST 61
QY 62 SIHHGFFQAGNWDGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
DB 62 SIHHGFFQAGNWDGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
QY 122 GPFVYDPRDPRHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 181
DB 122 GPFVYDPRDPRHASRYDVNDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 181
QY 182 TAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTVIEVDGINSQPLLVDLSIQIFA 241
DB 182 TADLSVLSVTPGKRYRFLVSVISCDPNYTFSDGHNLTVIEVDGINSQPLLVDLSIQIFA 241
QY 242 QRYSEVLNANOTVGNVWVRANPNFVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 301
DB 242 QRYSEVLNANOTVGNVWVRANPNFVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 301
QY 302 ETNLHPLARMPVPGSPPTGGVDKALNLFNFGTNNFNNATFTPTPVVLLQILSGAQ 361
DB 302 EVNLHPLVTTAVPGSPVAGGVDLAINMAFNFGTNNFNNATFTPTPVVLLQILSGAQ 361
QY 362 AQDLLPAGSVYPLPAHSTIETLTPATAPAGAPHPHHLGHAFVAVRSAGSTTYNNDPI 421
DB 362 AQDLLPAGSVYPLPAHSTIETLTPATAPAGAPHPHHLGHAFVAVRSAGSTTYNNDPI 421
QY 422 FRDVSSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 481
DB 422 FRDVSSTGTPAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 481
QY 482 KAWSDLCPYDGLSEANQ 499
DB 482 KAWSDLCPYDGLSEANQ 499

RESULT 10
US-09-993-318A-2

; Sequence 2, Application us/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Chery, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5998353 of No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York

COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,318A
FILING DATE: December 18, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-318A-2

Query Match 82.5%; Score 2201; DB 2; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
Qy 2 IGPVSLVAVNAPSPDGLRDAIVVNGVWSPDLITGKKGDRFQNLVNDLTNTHMLKST 61
Db 2 IGPVADLTITNAVSPDGSFQAVVNGTGPPLITGNMGDRFQNLVNDLTNTHMLKST 61
Qy 62 SIHWHGFFQAGTNWADGPAFVNOCPVQPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHWHGFFQKGTNADGPAFVNOCPVQPISSGHSFLYDFQVDPQAGTFWYHSHLSTQYCDGLR 121
Qy 122 GPFVYVDPKPHASRYDVNDNESTVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Db 122 GPFVYVDPNDAADLYDVNDNDVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Qy 182 TAALAVINVOHCKRYRFRFLVSLSCDPNPTFSIDGHNLFVIEVDGINSOPLLVDSIQIFAA 241
Db 182 TAALAVINVOHCKRYRFRFLVSLSCDPNPTFSIDGHNLFVIEVDGINSOPLLVDSIQIFAA 241
Qy 302 EVNLHPLVTAVPGSPVAGGVLDLAINMAFNENGTNFFINGASFTPTPTVLLQIISGAQN 361
Db 302 EVNLHPLVTAVPGSPVAGGVLDLAINMAFNENGTNFFINGASFTPTPTVLLQIISGAQN 361
Qy 362 AQDILLPGSVYSLPSNADIEISFATAAAGPAPHFHLGHAFVAVRSAGSTVYNDNPI 421
Db 362 AQDILLPGSVYSLPSNADIEISFATAAAGPAPHFHLGHAFVAVRSAGSTVYNDNPI 421
Qy 422 FRDVTSTGTPAAGNVITRFOTDNGPWFHLCHIDFHLDAFAIVAEADVADVAANVPV 481
Db 422 FRDVTSTGTPAAGNVITRFOTDNGPWFHLCHIDFHLDAFAIVAEADVADVAANVPV 481
Qy 482 KAWSDLCPYDGLSEANQ 499
Db 482 KAWSDLCPYDGLSEANQ 499

RESULT 11
us-09-399-886-2
; Sequence 2, Application US/09399886
; Patent No. 6140092

GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400920 No. 6140092disk of No. 6140092th America
STREET: 405 Lexington Avenue
CITY: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/399,886
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,318
FILING DATE: December 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-399-886-2

Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
Qy 2 IGPVSLVAVNAPSPDGLRDAIVVNGVWSPDLITGKKGDRFQNLVNDLTNTHMLKST 61
Db 2 IGPVADLTITNAVSPDGSFQAVVNGTGPPLITGNMGDRFQNLVNDLTNTHMLKST 61
Qy 62 SIHWHGFFQAGTNWADGPAFVNOCPVQPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHWHGFFQKGTNADGPAFVNOCPVQPISSGHSFLYDFQVDPQAGTFWYHSHLSTQYCDGLR 121
Qy 122 GPFVYVDPKPHASRYDVNDNESTVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Db 122 GPFVYVDPNDAADLYDVNDNDVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Qy 182 TAALAVINVOHCKRYRFRFLVSLSCDPNPTFSIDGHNLFVIEVDGINSOPLLVDSIQIFAA 241
Db 182 TAALAVINVOHCKRYRFRFLVSLSCDPNPTFSIDGHNLFVIEVDGINSOPLLVDSIQIFAA 241
Qy 242 QRYSFVLNANQVNYWRANPNFCTGVFAGINSAILRYOGAPVAEPTTTTQTSVIPLI 301
Db 242 QRYSFVLEANOAVDNYWRANPNFCTGVFAGINSAILRYOGAPVAEPTTTTQTSVIPLI 301
Qy 302 ETNLHPLARMVPVPGSPPTGGVDKALNLFNENGTNFFINATFTPTPTVLLQIISGAQT 361
Db 302 EVNLHPLVTAVPGSPVAGGVLDLAINMAFNENGTNFFINGASFTPTPTVLLQIISGAQN 361
Qy 362 AQDILLPGSVYSLPSNADIEISFATAAAGPAPHFHLGHAFVAVRSAGSTVYNDNPI 421
Db 362 AQDILLPGSVYSLPSNADIEISFATAAAGPAPHFHLGHAFVAVRSAGSTVYNDNPI 421

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Db 362 AQDLLPGSVYSLPSNADIEISPPATAAAGPAPHPHLLHGHAFVAVVRSAGSTVYNDNPI 421
QY 422 FRDVGSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKANPVP 481
Db 422 FRDVGSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKANPVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDGLDPSDQ 499

RESULT 12
US-09-396-260-2
; Sequence 2, Application US/09396260
; Patent No. 6184015
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6184015o No. 6184015disk of No. 6184015th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-396-260-2

Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.le-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;

QY 2 IGPVSLVAVAPSPDGLRDAIVVNGVSPSLITGKGRFQINLVVDLTNHSMLKST 61
Db 2 IGPVADLTITNAVSPDGRSQAVVNGGTGPGLTGNMGDFQINLVNDLTNHTMLKST 61
QY 62 SIHWGFFQAGTNWADGPAFYNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHWGFFQKGTNWDGPAFYNQCPISGHSFLYDFQVDAQGTFWYHSHLSTQYCDGLR 121
QY 122 GPFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRLGADATFLINGRSASTP 181
Db 122 GPFVYVDPNDPAADLYDVNDTDTITLVDWYHVAAKLGAFFPLGADATFLINGKGRSPST 181
QY 182 TAAIAVINQHKRYRFLVSLISCDPNFTFSDGHNLTVEVDGINSOPLLVDSIQIFAA 241
Db 182 TADLSVISVTPGKRYRFLVSLSCDPNFTFSDGHNMTIETDSTINTAPLVVDSIQIFAA 241
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Db 182 TADLSVISVTPGKRYRFLVSLSCDPNFTFSDGHNMTIETDSTINTAPLVVDSIQIFAA 241
QY 242 QYSFVLNANQTVGNVWVRANFNFTVGFAGGINSAILRYQGAPVAEPTTTQTTSVIPLI 301
Db 242 QYSFVLEANOAYDVNWIRANFNFTVGFAGGINSAILRYDGAAGAAVEPTTTQTSTAPLN 301
QY 302 ETNLHPLARMVPVPGSTPGGVKALNLAFNFTGTFNNATFTPTVPLVLIQLSGAQT 361
Db 302 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNFTGTFNNGASFTPTVPLVLIQLSGAQN 361
QY 362 AQDLLPAGSVYPLPAHSTIETILPATALAPGAPHPHLLHGHAFVAVVRSAGSTVYNDNPI 421
Db 362 AQDLLPAGSVYSLPSNADIEISPPATAAAGPAPHPHLLHGHAFVAVVRSAGSTVYNDNPI 421
QY 422 FRDVGSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKANPVP 481
Db 422 FRDVGSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKANPVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDGLDPSDQ 499

RESULT 13
US-09-576-281-2
; Sequence 2, Application US/09576281
; Patent No. 6277611
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Falle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6277611o No. 6277611disk of No. 6277611th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/576,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-576-281-2

Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.le-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
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QY 182 TAALAVINQHGKRYFRFLVSLSCDPNTFSIDGHNLTVIEVDGINSQPLLVDLSQIFAA 241
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DB 302 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNENGTNFFINGASFTPTVPVLLQIISGAQN 361
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DB 482 QAWSDLCPYDALDPSDQ 499

RESULT 14
US-08-462-484-2
; Sequence 2, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Iaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
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; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
; US-08-462-484-2

Query Match 82.2%; Score 2194; DB 1; Length 520;
Best Local Similarity 79.7%; Pred. No. 3.2e-189;
Matches 397; Conservative 36; Mismatches 65; Indels 0; Gaps 0;

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DB 23 IGPVADLITNAVSPDGFSGRAVVGVTGPGPLITGNMGDRFQNLNVVDLTNHSMLKST 82
QY 62 SIHWGFFQAGTNWADGPAFVNOCPISGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 121
DB 83 SIHWGFFQAGTNWADGPAFVNOCPISGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLR 142
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DB 143 GFVVYDNDPAADLYDVNDNDVTITLDWYHVAAKLGFAPFPLGADATLINGKRSPT 202
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DB 263 QRYSEVLEAQAVDNYWIRANPNFNGVGTGGINSAILRYDCAAAVEPTTTQTSAPLN 322
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DB 503 QAWSDLCPYDALDPSDQ 520

RESULT 15
US-08-441-147-2
; Sequence 2, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Iaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5770418o No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
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Search completed: December 14, 2002, 08:29:50
Job time : 29 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:07:51 ; Search time 60 Seconds
(without alignments)
7666.919 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gcatcgccgcggcgagag.....tgagcaggactaacagtgga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	771.8	51.5	2880	1	US-08-441-147-3
3	771.8	51.5	2880	5	PCT-US95-07536-3
4	519	34.6	1722	4	US-09-221-275-3
5	472.6	31.5	1170	3	US-08-689-421-20
6	472.6	31.5	1170	4	US-09-389-528-20
7	472.6	31.5	1170	4	US-09-181-827A-20
8	452.8	30.2	2418	1	US-08-462-484-1
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Sequence 26, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-462-484-3
; Sequence 3, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 56675310 No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185,010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron

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QY 1172 CGGTCGACGCGACCCCTTCCACCTGCACGGT----- 1203
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QY 1352 TCACATGCCACATCGATTTCCACCTCGACGCGGCTTCGCGATCGTTCGACGAGGACG 1411
Db 2344 TCACATGCCACATCGATTTCCACCTCGACGCGGCTTCGCGATCGTTCGACGAGGACG 2403
QY 1412 TTCGCGACGTCGAGGCGGCGAAACCGGTTCCGAAGCGTTCGCGACCTGTGCCGATCT 1471
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RESULT 2

US-08-441-147-3
; Sequence 3, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron
; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: intron
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; 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
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; NAME/KEY: intron
; LOCATION: 1499..1553
US-08-441-147-3
Query Match 51.5%; Score 771.8; DB 1; Length 2880;
Best Local Similarity 70.7%; Pred. No. 9.9e-164;
Matches 1463; Conservative 0; Mismatches 37; Indels 569; Gaps 10;
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QY 61 CTTCCGGATGCCATCGTGTCAACGCGTGGTCCCTTCCCGCTCATCACCGGAAGA-- 118
Db 484 CTTCCGGATGCCATCGTGTCAACGCGTGGTCCCTTCCCGCTCATCACCGGAAGAAG 543
QY 119 -----AGGGAGACCGCTTT 131
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QY 132 CCAGCTCAACGTCGTCGACACCTTGACCAACACACAGCAGCTCTCAAGTCCAGTAGTATC-- 189
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QY 310 -----GGAA 313
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Db 1084 GTTGACCGACTGTTACACACCGCTCGCCGCGCTCGGTCGACGTTCCCA----- 1143
QY 490 -----CTCGGCGGACGCCA 505
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QY 506 CGCTCATCAATGTTGTTGGGCGGTCCACTCCACCGCGCTGCTGTGATCA 565
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Db 1264 ACGTCCAGCAGGAAAGCGGTGAGCATCTCTTGTATGCGCATTTCAATGCTTTGTGCTG 1323
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Db 1324 ACCTATCGGAACCGGAGTACCGCTTCCGCTCGTTGCTGATCTCGGACCGGAACTA 1383
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Db 1444 GCCTCTCCTGCTGACTATATCCAGATCTTCGCGCGGAGCGGCTACTCTCTCTGTTGTAAG 1503
QY 741 -----GTTGATCGGA 751
Db 1504 TCCGTGGCTGTCGATGCTCCAAAGTGGCGCTCACTCATATATTTGCTGATGTAAGTGGGA 1563
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QY 812 CCGGGGGGATCACTCGGCCATCTGCGCTACCAAGGCGCACAGTCCGCGGAGCCCACTA 871
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QY 872 CGACCCAGACGCTCGGTGATCCGCTATCGAGAGCACTTCACCCCTCGCTCGCA 931
Db 1684 CGACCCAGACGCTCGGTGATCCGCTATCGAGAGCACTTCACCCCTCGCTCGCGCA 1743
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QY 939 -----GCTTGGGAGCCGACACCGCGGGGCGTGCAGAGGCGCTCAACCTCGCG 987
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QY 997 -----AAGCGGACCAACTCTTCTATCAACAACGCGGACTTTTCAACGCGCGGCGGCTCGCGG 1051
Db 1924 TTCAGAACGGGACCAACTCTTCTATCAACAACGCGGACTTTTCAACGCGCGGCGGCTCGCGG 1983
QY 1052 TACTCTCTCAGATCTGAGCGGTGGCGAGACCGGACCAAGACCTGCTCCCTCGAGGCTCTG 1111

Db 1984 TACTCTCTCAGATCTGAGCGGTGCGCAGACCGCAAGACCTGCTCCCGCAGGCTCTG 2043
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Db 2044 TCTACCGGCTCCCGGCCACTCCACCATCAGATCAGCTGCGCGGACCGCTTGGCCC 2103
QY 1172 CGGGTGACCGCGACCCCTTCCACCTGCACGGT----- 1203
Db 2104 CGGGTGACCGCGACCCCTTCCACCTGCACGGTGTATGTTCCCTGCTGCTTCCCTTCTTATC 2163
QY 1204 -----CACGGCTTCGCGGCTGTTTCGCGAGCGCG 1231
Db 2164 CCGGAACAGTGTCTCAGTCCGTCCTCCATCAGCAGCGCTTCGCGGTTTCGCGAGCGG 2223
QY 1232 GGAGCACACGTTAATCTACAAGCAGCCGATCTTCCGCGACGCTCGTGAGCACCGGACGC 1291
Db 2224 GGAGCACACGTTAATCTACAAGCAGCCGATCTTCCGCGACGCTCGTGAGCACCGGACGC 2283
QY 1292 CCGCGCGGCGGACAGCTCAGCATCCGCTTCAGAGCGGACAAACCGCGGCGCTGTTCC 1351
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Db 2344 TCCACTGCCACATCGACTTCCACTCGACGCGGCTTCGCGATCGTTCGCGAGGAGCG 2403
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RESULT 3

PCT-US95-07536-3
; Sequence 3, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

Db 1440 GCA---CTGATGCGAAGCAGCAACCTCATTTCGCTTCGTGACCGACACCCAGGCCGCT 1496
QY 1346 GGTTCCTCCACCTCCACATCGACTTCCACTCGACCGGGCTTCGGATCGTGTTCGCAG 1405
Db 1497 GGTTCCTCCACCTCATATGATGATGTCATCTCGAAATTCGCTGCTGCTTCGCGCG 1556
QY 1406 AGACCTGTCGGACGTGAAGGGCGGCAACCCGGTTCGGAAGGGCTGGTCGGACCTGTGCC 1465
Db 1557 AAGACGTGACATCCATTTCGGCCCC-----ACCTCGCGGTGGGACGACTTGTGCC 1607
QY 1466 CGATCTACGACGGCTGACGGAGGCTAACCACTGA 1500
Db 1608 CCATATATGATGCTTTGAGCGCAACAGCAAAAGGA 1642

RESULT 5

US-08-689-421-20
; Sequence 20, Application US/08689421
; Patent No. 6008029
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6008029o No. 6008029disk of No. 6008029th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,421
; FILING DATE: 9-Aug-1996
; CLASSIFICATION: A35
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4554.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1170
US-08-689-421-20

Query Match 31.5%; Score 472.6; DB 3; Length 1170;

Best Local Similarity 65.0%; Pred. No. 5.5e-97;
Matches 770; Conservative 0; Mismatches 394; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGCTTCTCCAGGACGACCAACTGGGACAGGACCCCGCTTCGTCAC 249
Db 1 CACTGGCAGCGCATGTTCGAAGGGGAGCTGCCTGGGCTGATGGTCTCTGCTGGCGTCAC 60
QY 250 CAGTGGCCCTATTGCTTCCGGGATCATTTCTGTACGACTTCATGTGCCGCCACAGGCA 309
Db 61 CAATGCCCTATTTCGCCAGGCGATTCGTTCTGTGTACAAAGTTCAGGCTCTTAACCAAGCC 120

QY 310 GGAACGTTCTGTGTACACAGTCTATCTGTCTACGCAATACTGTGACGGGCTCGAGAGACCG 369
Db 121 GGTACTTTCTGTGTACACCTCCCATCAGAAATCGCAATATGTGACGGTTTGGTGCGGCT 180
QY 370 TTCTGCTGTGTACGACCCCAAGGATCGGACGCGGCTACGATGTTGACAAACAGAGAC 429
Db 181 ATGGTGTATATGACCCAGCTCGACCCACATCGCAACTTGTATGACATTGACAAACAGAGCC 240
QY 430 AGGTCATACGTTGACCGACTGTGTACACACCGCTGCGCGGGCTCGGTGCCAGTTCCCA 489
Db 241 ACATCATTTACGTCGACACTGGTATACGTCCTGC---TCCCTCTGCAAGTCTCGTT 297
QY 490 CTCGGCGGACGCGACGCTCATCAATGCTTTGGGCGGTTCGGCCCTCCACTCCACCGCC 549
Db 298 CCCACCCAGATTCACGCTTATCAACGGTAAGGGCCGGTATGCTGGTGGCCCTACCGTA 357
QY 550 GCGCTTGTGTGATCAACGCTCCAGCACGCGGAAAGCGGTACCGCTTCGCTCTCGTTTCGATC 609
Db 358 CTTCTCGCGTCTATTTCTGAACCCGAAACCGACGATACCGGTTCCGCTTCCCTT 417
QY 610 TCGTCGACCGCGAATACAGCTTCAGCATCGAGGCGCAATCTGACCGTCTCATCGAGTTC 669
Db 418 TCATGGATCTTAATATGTTCTCTATCGATGGGCATACCATGACTGTTATTGAGGTC 477
QY 670 GACGCTATCAACGCGACGCTCTCTCTTGTGCACTCTATCCAGATCTTCGCGCGGACGCG 729
Db 478 GACGAGTTAAGTCCCAACCTCTCTGTGTGACTCGATCCAGATCTTCGAGGTGAGCGC 537
QY 730 TACTCTTGTGTGATGGAACGAAACGCGTGGCAACTACTGTGGTTCGCGGCAACCG 789
Db 538 TACTCTTGTGTGATGGAACGAAACGCGTGGCAACTACTGTGGTTCGCGGCAACCG 597
QY 790 AACTTCGGAACGCTTGGGTTTCGCGGGGGATCAACTCGCGCATCTCTGCGCTACCAAGC 849
Db 598 ACATCGTACTACGGGCTTCGCTGGTGGATCAATCTGCGATTCTGCGTATGTGGC 657
QY 850 GCACGAGTCGCGGAGCCCACTACGACCCAGACGACGCTCGGTGATCCCGTCTATTCGAGACG 909
Db 658 GCTTCAATACAGACCCCACTACCAACAACTCTCTTCAGCAACCTCTCTCTGAGACC 717
QY 910 AACTTCACCCCTCGCTCGCATGCTGTGCTGCGGAGCGCGGACCCGCGGCGGCTCGAC 969
Db 718 AATCTCCACCCCTTGACCAACCTGCTGCTGCGGTTGCTTACCCAGGTGGCGTCGAC 777
QY 970 AAGGCGCTCAACCT-----CGCGTTTAACTTCAACGGCAGCAACCTTCTTCATCAACAAC 1023
Db 778 GTCGCGATCAACCTTAACAGGTTATTCGATTTCAGTAGTCTCACCTTCTCCGTTAACGGA 837
QY 1024 GCGCTTTCACGCGCGGACCGCTTCGCGGTACTCTCCAGATTCTGAGCGGTGGCGAGACC 1083
Db 838 GCGCTTTCATCAACGCGCGGCTCTGCTGCTTTCAGATCATGAGCGGTGACAGACT 897
QY 1084 GCAGAGACCTGCTCCCTGCAGGCTCTGTCTACCCGCTCCGCGGACCTCCACCATCGAG 1143
Db 898 GCCAGACGCTCTTCTCCCTCGGTTTCGCTGCTAGTCTCTTCCCGGTAAACAAAGTATCGAG 957
QY 1144 ATACGCTTCGCGGACCGCTTGGCGCGGCTGACCCGACCCCTTCACCTTCGACCGGT 1203
Db 958 CTTTCTATGCTGGAGGC-----TCCACTGGCAGTCCCATCCCTTCCATCTCCAGGT 1011
QY 1204 CAGCGCTTCGCGGTCTGTCGAGCGCGGAGACCACTGATATACATACAGACCGCGATC 1263
Db 1012 CAGCAATTTGCTGTGTGAGAGCGCGGAGTTTCAGCTTCAACCTTCGCAACCGCGTA 1071
QY 1264 TTCGCGGAGCTGTGAGACGCGGACGCGCGCGCGGGGAGCAACCTGACGATCCGCTTC 1323
Db 1072 CGCAGGATGTGCTGAGTCCCG-----TGTTGCTGGTGACAACTGACCATTCGATT 1125
QY 1324 CAGACGCAACCCCGCGGCGGTGTTCTTCCACTGCGACATCGAC 1368
Db 1126 CGTACCGATTAACCTGGACCATGGATTCTCCATTGCGCATATCGAC 1170

;; TITLE OF INVENTION: Acids Encoding Same
;; FILE REFERENCE: 4534.200-US
;; CURRENT APPLICATION NUMBER: US/09/181.827A
;; CURRENT FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/002.800
;; PRIOR FILING DATE: 1995-08-25
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20
;; LENGTH: 1170
;; TYPE: DNA
;; ORGANISM: Coprinus cinereus
US-09-181-827A-20

Query Match 31.5%; Score 472.6; DB 4; Length 1170;
Best Local Similarity 65.0%; Pred. No. 5.5e-97;
Matches 770; Conservative 0; Mismatches 394; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGCTTCTCCAGGAGGACCACTGGGCAGACGAGCCGGCTTCGTCAAC 249
Db 1 CACTGGCAGCGCATGTTCAAAGGGGAGCTGCCTGGGCTGATGCTCGTGGCTCACC 60
QY 250 CACTGGCCCTATTGCTCCGGGCTATTCATTTCTGTACGACTTCCATGTGCCCGACGAGCA 309
Db 61 CANTGCCCTATTTCGCCAGGGCATTCGTTCTGTACAAAGTTCCAGGCTCTTAACAGCC 120
QY 310 GGAACGTTCTGGTACCACAGCTATCTGTCTACGCAATCTGTGACGGGCTCGGAGGACCG 369
Db 121 GGTACTTTCTGTGTTACCACTCCCATCAGCAATTCGATATTTGACGGTTTTCGCTGGGCT 180
QY 370 TTGTCGTGTACGACCCCAAGGATCCGACGCGCCAGCGCTACGATTTGACACGAGAGC 429
Db 181 ATGTCGTGTATGACCCAGTTCGACCCACATCGCAACTTGTGATGACATTTGACAAACGAGCC 240
QY 430 ACGGTCTATCAGTTGACCGAGTGTACACACCGCTGCCCGGCTCGGTCCCGAGTTCCCA 489
Db 241 ACATCATATTAGCTCGAGACTGTATCAGTCCCTGC---TCCCTCTGAGGTCTCGTT 297
QY 490 CTGGCGGCGGACGCGCTCAATAGTCTTTGGGGGCTGGGCTTCCCTCACTCCACGCGC 549
Db 298 CCGACCCGAGATTCCAGCTTATCAACGTTAAGGGCGGTATGCTGGTGGCCCTACCGTA 357
QY 550 GCGCTTGTCTGTATCAACGTCACGACGCGGAAAGCGTACCGCTTCCGCTCTCGTTTCGATC 609
Db 358 CTTCTCGCGTCAATTTCTGTAAACCGGAAACCGAGATACCGGTTCCCGCTTGTTCCTT 417
QY 610 TCTGCGACCCGACACTACAGTTTACGATCGACGGGACAACTCTGACCGTCTATCGAGGTC 669
Db 418 TCATGCGATCCTAATTATGTTATCTCTATCGATGGGCATACCATGACTGTTATGAGTTC 477
QY 670 GAGGTATCAACAGCCAGCTCTCTTGTGACTCTATTCAGATCTTTGGCGGCGGACGCG 729
Db 478 GACGGAGTTAAGCTCCAACTCTCTGTGTGACTCGATCCAGATCTTCGAGGTCAGCGC 537
QY 730 TACTCTTGTGTGTTGAATGGAAACCAACGCTGCGCAACTACTGGGTCCGCGCAACCCG 789
Db 538 TACTCTGTTCTTCAACGCCAACCCCGCCGCTCGGAACCTACTGGGTGCGAGCAACCCC 597
QY 790 AACTTCGGAACGGTTGGTTGCGCGGGGATCAACTCCGCCATCTCGCTACCAAGGC 849
Db 598 AACATCGGTACTACGGCTTCGTCGGTGGAGTCAATTCGCGATTCTGCGCTATGTGGC 657
QY 850 GCACAGTCCCGGAGCCACTAGCCAGACGACGCTGGTGTATCCGGCTTATCGAGAGC 909
Db 658 GCCTCCAATACAGACCCCACTACCAACCTCTTTCAGCAACCCCTCTCTCTTGAGACC 717
QY 910 AACTTGACCCCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCCGGGGCGTCGAC 969
Db 718 AATCTCCACCCCTTGACCAACCCCTGTGCTCTCTGCTTCCCTACCCAGGTGCGCTGAC 777
QY 970 AAGCGCTCAACCT-----CGCGTTTAACTTCAACGGCACCACCACTTCTTCATCAACAAC 1023
Db 778 GTCGCGATCAACCTTAACAGGTTATTCGATTTTCAGTAGTCTCACCTTCTCCGTTAAGCA 837

QY 1024 GCACCTTTACGCGCGCGACCGTCCCGGTACTCTCCAGATTTCTGAGCGGTGCGAGACC 1083
Db 838 GCCACTTTCCATCAACCGCGCGTCCCTGTCTTCTTCCAGATGAGCGGTGCGAGACT 897
QY 1084 GCACAAGACCTGCTCCCTCCAGGCTCTGTACCCGCTCCCGGCCCACTCCACCATCGAG 1143
Db 898 GCCAGCAGCTTCTCCCTCCGTTCCGTTAGCTCTCCCGGTACCAAGTCAATCGAG 957
QY 1144 ATCAGCTGCCGCGGACCGGCTTGGCCCGGCTGACCGCACCCCTTCCACCTGCGAGGT 1203
Db 958 CTTTCTATGCTCGAGGC-----TCCACTGGCAGTCCCATCCCTTCCATCTCCAGGT 1011
QY 1204 CACGCTTCCGCGTCTGCTGACGCGGGGAGCACACGCTATTAACATCAACAGCCGATC 1263
Db 1012 CACGAATTTCTGCTGTGAGAGCGGGGAGTTGACCTTACAACTTCGCGAACCAGGTA 1071
QY 1264 TTCGCGGACGCTGTGACGAGCGGACGCGCGCGGCGGCGGACAGCTGACAGTCCGCTTC 1323
Db 1072 CGAGGAGTCTGTGAGTGCCG-----TGTGCTGGTGACACGTCACCATTCGATTTC 1125
QY 1324 CACAGGACAAACCCCGCGGCTGCTTCTCCACTGCCACATCGAC 1368
Db 1126 CGTACCGATTAACCTGGACCATGATTTCTCCATTTGCCATATCGAC 1170

RESULT 8

US-08-462-484-1
; Sequence 1, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboe, Henrik
; APPLICANT: Schneider, Palte
; APPLICANT: Aslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowrey, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

Db	1738	ATCAAGCGGACGTCCTTTCACAGCCCGCCCGAGACCGTGCTGCTCTCCAGATCATCAGCGGC	1739
QY	1075	GCGCAGACGCGCAAGAACCTGCTCCCTGCAGAGCTCTGTCTACCCGCTCCCGGCCCACTCC	1134
Db	1798	GCGCAGAACGCGCAGGACCTCTCTGCCCCTCGGTAGCGTCTACTCGCTTCCCTCGAAGCGCC	1857
QY	1135	ACCATCGAGATCAGCTGCTCCGCGGAGACCGCTTGGCGCCCGGGGTGACCGCACCCCTTCAC	1194
Db	1858	GAGATCGAGATCTCTCTCCCGCCACACCGCGCGCCCGCGCTGCGCCCGCACCCCTTCAC	1917
QY	1195	CTCGACGGTTCACGCCCTTCGCGGTTCGTCGACGCGGGGAGCACCACCTATAACTACAAAC	1254
Db	1918	TTGCAGCGGCACGCGTTCGCGGTCTCGCGACGCGCGCGCAGCAGCGTTTACAACTACGAC	1977
QY	1255	GACCCGANTCTTCGCGACCTCGTGAGCAGCGGCACGCGCCGCGGGGGGACAGCGTCAG	1314
Db	1978	AACCCCATCTTCGCGACGCTCTGACGACGGGGAGCGCTCGGGCGGTGACAACTCACC	2037
QY	1315	ATCCGCTTCCAGACGACAAACCCCGCGCGCTGGTTCCTCCACTGCGACATCGACTTCCAC	1374
Db	2038	ATCCGCTTCGCGACCGACAACCCCGCGCGTGTCTCTCCACTGCCACATCGACTTCCAC	2097
QY	1375	CTCGACGCGGGCTTCGCGANTCGTGTTCGCGAGAGAGCTGTTCGGAGCTGAAGCGCGCGAAC	1434
Db	2098	CTCGAGCGCGCTTCGCGCTCGTGTTCGCGGAGGACATCCCGGACGTGCGCTCGGCGAAC	2157
QY	1435	CCGGTTCGGAAGCGTGGTCGGACCTGTCCCGCATCTACGACGGGCTCAGCGAGCTAAC	1494
Db	2158	CCGTCGCCCGAGCGTGGTTCGAGCTCTGTCGACCTACGACCGCTCGACCGGCGAC	2217
QY	1495	CAGTGA 1500	
Db	2218	CAGTAA 2223	

RESULT 9

US-08-441-147-1 ~

; Sequence 1, Application US/08441147

; Patent No. 5770418

; GENERAL INFORMATION:

; APPLICANT: Xu, Feng, Debbie Sue

; APPLICANT: Xu, Feng

; APPLICANT: Dalboe, Henrik

; APPLICANT: Schneider, Palle

; APPLICANT: Aslmyer, Dorrit A.

; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, I

; STREET: 405 Lexington Avenue, Suite 6400

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,147

; FILING DATE: 15-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney, Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4185.010-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 867 0123

; TELEFAX: 212 878 9655

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
; FEATURE:
;   NAME/KEY: intron
;   LOCATION: 414..464
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 534..589
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 710..764
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 879..934
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 1001..1050
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 1147..1197
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 1354..1410
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 1609..1662
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: join (413..465, 533..590, 709..765, 878..935)
;   LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
; US-08-441-147-1

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Query Match 30.2%; Score 452.8; DB 1; Length 2418;

Best Local Similarity 69.0%; Pred. No. 1.7e-92;

Matches 708; Conservative 0; Mismatches 207; Indels 111; Gaps 2;

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QY 586 TACCGCTTCGCTCGCTTCGATCTCGTGGACCGGACACGATACAGTTTCAGCATCGAGGG 645
Db 1198 TACCGTTTCGCTGGGTGCTCGTGGACCGGACACGATACAGTTTCAGCATCGATGGT 1257
QY 646 CACAATCTGACCGTTCATCGAGGTCGAGGTATCAACAGCGAGGCTCTCTTGTGACTCT 705
Db 1258 CACAACATGACGATCATCGAGACGACTCAATCAACAGCGGCGCCCTCGTCTGACTCC 1317
QY 706 ATCAGATCTTCGCGCGGACGCTACTCTCTTGTGTGA----- 745
Db 1318 ATTCAGATCTTCGCGCGGACGCTACTCTCTGTTGTAAGTTCGATTCATCTCTAAAG 1377
QY 746 -----ATCGGAACCAACGCTCGCAAC 768
Db 1378 TTGGTCGCTGTAGTATCTATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1437
QY 769 TACTGGTTCGCGGAACCGAATTCGGAAACGTTGGTTCGCGGGGGGATCAACTCC 828
Db 1438 TACTGGATTTCGCGCAACCGAATTCGGTAACGTCGGGTTTACCGCGCGCATTAACGTCG 1497
QY 829 GCGATCTGCGCTACCAAGCGGACACGATGCGGAGCGGCTAGGACCGACGAGCTCG 888
Db 1498 GCGATCTGCGCTACCAAGCGGACACGATGCGGAGCGGCTAGGACCGGACGAGCTCG 1557
QY 889 GTGATCCCGCTTATCGAGAGCAACTTGCACCCCTCGCTCGCATGCTGT----- 938
Db 1558 ACTGCGCGCTCAACGAGGTCAACCTGACCCGCTGTTACACCGCTGTGGTATGTAAT 1617
QY 939 -----GCGTGCAGCCCGGACA 954
Db 1618 ATTGTGGTAAATGTAATACATTTGTTGTAACCTCGACCCCGGACGCTGCTCGCGGTC 1677

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QY 955 CCGGGGCGCTCGACAGGCGCTCAACCTCGCGTTTAACTTCAACGCGCACCACTTCTTC 1014
Db 1678 GCTGGTGTGTGACCTGGCCATCAACATGCGGTTCACCTTCAACGCGCACCACTTCTTC 1737
QY 1015 ATCAACAACGCGACTTTTCAGCGCGCGGACCGTCCCGGTACTCTCTCCAGATTTCTGAGGGT 1074
Db 1738 ATCAACGCGACGCTTTTCAGCGCGCGGACCGTCCCGGTACTCTCTCCAGATCATCAGCGG 1797
QY 1075 GCGCAGACCGCACAAGACCTTCTCCCTGCGAGGCTCTGTCTACCGGCTCCGCGGCGCATCC 1134
Db 1798 GCGCAGAACGCGCAGGACCTCTCTCCCTGCGGTAGCGTCTACTGCTTCCCTCGAAGCGC 1857
QY 1135 ACCATCGAGATCAAGCTTCCCGGACCGCTTGGCCCGCGGTGACCGCACCCCTTCCAC 1194
Db 1858 GACATCGAGATCTCTTCCCGGACCGCTGCGCGCGCGGCGCGGCGCGGCGCGGCGCGGCG 1917
QY 1195 CTGACGCTTCAGCGCTTCGCGGCTGTTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 1254
Db 1918 TTGCACGCGCAGCGCTTTCGCGGCTGTTCCGCGAGCGCGGCGGCGGCGGCGGCGGCGGCG 1977
QY 1255 GACCCGATCTTCGCGGACGCTGTCGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1314
Db 1978 AACCCCATCTTCGCGGACGCTGTCGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2037
QY 1315 ATCCGCTTCCAGACGGAACCCCGGCGGCTGTTCCCTCCACTGCCACATCGACTTCCAC 1374
Db 2038 ATCCGCTTCCGACCGGACACCCCGGCGGCTGTTCCCTCCACTGCCACATCGACTTCCAC 2097
QY 1375 CTGACGCGGCGCTTCGCGATGCTGTTGCGAGAGGACGCTTCCGAGCGTGAAGGCGGCGAAC 1434
Db 2098 CTGAGGCGCGCTTTCGCGGCTGTTCCGCGAGGACATCCCGACGTCGCGGCGGCGGCGGCG 2157
QY 1435 CCGGTTCCGAGGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCT 1494
Db 2158 CCGTCCCGGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCTGTCGCGGCT 2217
QY 1495 CAGTGA 1500
Db 2218 CAGTAA 2223

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RESULT 10

PCT-US95-07536-1

; Sequence 1, Application PC/TUS9507536

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

; NUCLEIC ACIDS ENCODING SAME

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.

; STREET: 405 Lexington Avenue, Suite 6400

; COUNTRY: U.S.A.

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/07536

; FILING DATE: 15-June-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/265,534

; FILING DATE: 24-June-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney, Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4185.204-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 867 0123

; TELEFAX: 212 878 9655

Query Match	30.2%	Score 452.8;	DB.5;	Length 2418;
Best local Similarity	69.0%;	Pred. No. 1.7e-92;		
Matches 708;	Conservative 0;	Mismatches 207;	Indels 111;	Gaps 2;
QY	586	TACCGCTCCGCTCGCTTTTCGATCTCGTGGCACCGCAACTACAGTTCAGCATCGAGGG	645	
Db	1198	TACCGTTTCGCGCTGGTCCCTGCTGCGACCCCACTACAGTTCAGCATCGATGCT	1257	
QY	646	CACAATCTGACCGCTATCGAGGTCGACGGTATCAACAGCCAGCTCTCCTTGTTCGACTCT	705	
Db	1258	CACAACATGAGCATCATCGAGACCGACTCAATCAACAGCGCGCCCTCGTCTGGACTCC	1317	
QY	706	ATTCAGATCTTCGCGGCACGCGTACTCCTTTGTGTGA-----	745	
Db	1318	ATTGAGATCTTCGCGGCCACGCTTACTCCTTCGTGGTAACTTCGATTATCCTCTTAACG	1377	
QY	746	-----ATGGAACCAACAGCTCGGCAAC	768	
Db	1378	TTGGTCGCTGTTAGTGATCGTATGGTCATGTAGCTCGAGGCCAACAGGCCGCTCGACAA	1437	
QY	769	TACTGGGTCCGCGGAACCCGAACCTTCGGAACGTTGGGTTTCGCGGGGGGATCAACTCC	828	
Db	1438	TACTGGATTCCGCGCAACCCGAACCTTCGGAACGTTGGGTTTCGCGGGGATCAACTCG	1497	
QY	829	GCCATCTTCGCGCTACCAAGGCGCACAGTCCGCGAGCCCACTACGACCCAGACAGCTCG	888	
Db	1498	GCTATCTTCGCTACGATGTTGCGGCTGCCGTGGAGCCCAACCAACCAACCAACCGTCG	1557	
QY	889	GTGATCCGCGCTATCGAGACCAACTTCGACCCCTTCGCTCGCATGCCCTGT-----	938	
Db	1558	ACTGGCGCGCTCAAGAGGTCACACTGTCACCCCGCTGGTTACCCGCTGTGGTATGTAAT	1617	
QY	939	-----GCCTTGGACGCCCGACA	954	

Db	1618	ATTGTCGGTAATGAATACATTGTTCTGACCTTCGACCCACACCGCTGGCTCGCCCGCTC	1617
Qy	955	CCCGGGGGCGTCGACAAAGGGCTCAACCTCGGCTTTAACTTCAACGGCACCAACTTCTTC	1014
Db	1678	GCTGGTGGTCTGCACCTGGCGCAATCAACATGGCGGTTCAACTTCAACGGCACCAACTTCTTC	1737
Qy	1015	ATCAACAACCGCACTTTCACGCGCGCGACCGCTCCCGGTACTCCTCCAGATTCTGAGCGGT	1074
Db	1738	ATCAACGGCACGTCTTTCAGCGCCCGACCGTGCCTGTCTGCTCCAGATCATCAGCGCG	1797
Qy	1075	GCAGCAGACGACGACAGACCTGTCTTCCTGAGGCTGTGTCTACCCGCTCCCGGCCCACTCC	1134
Db	1798	GCAGCAGAACGCGCAGGACCTCTCTGCCCTCCGGTAGCGTCTACTCGCTTCCCTTCGAACGCC	1857
Qy	1135	ACCATCAGATACAGCTGCCCGCGACCGCTTGGCCCGGGTGACCGCACCCCTTCAC	1194
Db	1858	GACATCAGATCTCTCTCCCGCCACCGCGCGCCCGCTGGCGCCACCCCTTCAC	1917
Qy	1195	CTGCACGCTCACGCTTCGCGGCTGTTCGACGCGGGGAGACCAACCGTATAACTACAC	1254
Db	1918	TTGCACGGCACCGTTCGCGGCTGCTCCGACGCGCGCAGCAGCGTTTACAACTACGAC	1977
Qy	1255	GACCCGATCTTCGCGACGTGTGTAGCAGCGGACACCGCCCGCGGGCGACAACTGACG	1314
Db	1978	AACCCCATCTTCCGCGACGTCTGCACGCGGGAGCGCTTCGCGCGCGGTGACAACTGAC	2037
Qy	1315	ATCCGCTTCCAGACGGACAAACCCCGCGCTGGTCTCCTCACTGCCACATCGACTTCCAC	1374
Db	2038	ATCCGCTTCCGACCCGACAAACCCCGCGCTGGTCTCCTCACTGCCACATCGACTTCCAC	2099
Qy	1375	CTGCACGCGGCTTCGCGATCTGTGTTCGACGAGAGCTTTCGCGAGCTGAAGCGCGCGAAC	1433
Db	2098	CTCGAGGCGGCTTCGCGCTGTGTTCGCGAGGACATCCCGAGCTCGCTCGCGCGAAC	2157
Qy	1435	CCGCTTCGAGGCGTGTGCGACCTGTGCCCGATCTACGACGGCTGAGCGAGGCTAAC	1494
Db	2158	CCGCTGCCCGAGGCTGTGCGACCTGTGCCCGATCTACGACGGCTGAGCGAGGCTAAC	2217
Qy	1495	CAGTGA 1500	
Db	2218	CAGTAA 2223	
RESULT 11			
US-08-689-421-22			
; Sequence 22, Application US/08689421			
; Patent No. 6008029			
; GENERAL INFORMATION:			
; APPLICANT: Yaver, Debbie S.			
; APPLICANT: Brown, Kimberley M.			
; APPLICANT: Kauppinen, Sakari			
; APPLICANT: Hakler, Torben P			
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS			
; TITLE OF INVENTION: ENCODING SAME			
; NUMBER OF SEQUENCES: 36			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: No. 6008029o No. 6008029disk of No. 6008029disk of America, 1			
; STREET: 405 Lexington Avenue, 64th Floor			
; CITY: New York			
; STATE: New York			
; COUNTRY: United States of America			
; ZIP: 10174-6401			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/689,421			
; FILING DATE: 9-AUG-1996			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Harrington, James J.			


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; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1161
US-09-389-528-22

Query Match      29.3%; Score 439.6; DB 4; Length 1161;
Best Local Similarity 63.4%; Pred. No. 1.3e-89;
Matches 746; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGTTCTCCAGCAGGACCAACTGGGCGAGACGACCGCGCTTGGTCAAC 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CACTGGCAGCGTTCTTCGAGGAGGTTACAGTTGGGCGGACGGTCTCTCGGGGTGTTACT 60

QY 250 CAGTGCCTATTGCTTCGGGCAATTCATTCTGTACGACTTCCATGTCCCGACAGCA 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CAATGCCCATTTGCCCTTGGTCACTCTTCTCTATAAGTTCCAGGCCAAAACCAAGCT 120

QY 310 GGAAGCTTCTGGTACCACAGTCATCTGTCTAGCCAATCTGTACGGGCTGCGAGACCG 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GGTACTCTGTGTACCAATCCACACATGTCAGTATTTGTAGGGCTTGAGAGGCGTC 180

QY 370 TTCGTGCTAGCAGCCCAAGGATCCGACGCCAGCGGTACGATGTGACAAACGAGGC 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATGGTGGCTTTACGATCCCTTAGATCCCATCTCTTCTCTATAAGTTCCAGGCCAAAACCAAGCT 240

QY 430 AGGGTGCATCAGCTTGACCGACTGTACCAACCGCTGCCCGGCTCGGTCCCAAGTCCCA 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACTATCATCAGCTCGCGACTGGTATACGATCCGAGGCGGTTTACCCAGGCGGACCGTCGTC 300

QY 490 CTCGGCGCGAGCGCCACGCTCATCAATGTCTTTGGCGGCTCGGCTCCACTCCCAACCGCC 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ACCCCCTGG---TCGACTTTGATCAATGCAAGGCGGTTACCCAGGCGGACCGCTCGTG 357

QY 550 GGGCTTGTGTGATCAAGTCCAGCAGCAAGAGCGCTACCGCTTCGGTCTCGTTTCGATC 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 CCCTTGGCGCTGATTACAGCTCAGCGCGGGAAGCGCTACCGCTTCGGCTCGTCTCCCTT 417

QY 610 TCGTGGAGCCCAACTTACAGCTTACAGCTCAGCGGCAAACTCTGACGCTCATCAGAGTC 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 TGTGGACCCCTAACTATGTATCTTCTATTGACGCTCACACCATGACGGTCAATGAAGTC 477

QY 670 GAGGTTCAACAGCGAGCGCTCTCTCTGTGCTACTCTATCCAGATCTTCCCGCGGAGCGC 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 GATGGTGTCAACCATGAACCGTTGGTTGTGACCACTTCAAATCTTCTGCTGTCAACGG 537

QY 730 TACTCCTTTGTGTTGAATCGAACAACGCTGCGCACTACTGGTTCGCGCGCAACCG 789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 TACTCCTTTGTGTTGAACCGCAACCGCGCGCGCTCAACACTACTGGTCAAGGCTAACCC 597

QY 790 AACTTCGGAACGGTTGGTTTCGCGGGGGATCAACTCCGCCATCCTGCGCTTACCAAGGC 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 AACCTCGGCTCTGCGGCTTGGTGGCGGTATTAATTTCCGCAATCTCGGATATGTTGA 657

QY 850 GCACAGTCCCGAGCCCACTAGGACCCAGACGCTCGGTATCCCGCTTATCCAGAGC 909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 GTCTCTCGGTCGACCAACCACTCCCAATTGCCATTTCAGCAACCCACTCTCCGAGAC 717

QY 910 AACTTCACCCCTCGCTCGCATGCTGTGCTTGGCAGCCGACCGCGGCGGCGCTCGAC 969
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 AACTTCACCCCTCTGTAATCCTGTGCACTGCGGCGGCGCTTCCCGCGGCTGACGTCGAT 777

QY 970 AAGGCGCTCAACCTCGGTTTAACTTCAACGGCAC-----CAACTTCTTCAATCAACAC 1023
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 778 GTCGCCATCAACCTGGATATCTTGTTCGACGCTCTCAATCCTCAAGTCTACTGTCAACGGT 837

QY 1024 GCACATTTACGCGCGGCGGCTCGGCTACTCTCTAGATCTGAGCGGTGCGGAGAC 1083
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 GCTACCTTGGATGAACACCCGTTTCGGGTCTCTCTCCAGATTTGAGCGGTGCAATACC 897

QY 1084 GCACAAGACCTGCTCCTCGAGGCTCTGTCTACCCGCTCCCGGCCCACTCCACCTGAGC 1143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 898 GCCTCATCTCTTCTCCCTCTGCGAGCGCTACACTCTTCCCGCTTAAACAGGTCATTGAG 957
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QY 1144 ATACAGCTGCCCGACCGCTTGGCCCCGGGTGCACCGACCCCTTCCACCTCCACGGT 1203
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Db 958 CTCCTATTCCCGGTGGTGTAT-----CGGTGCTCTACCCCATCCATCTTCAGGC 1011

QY 1204 CACGCCCTTCGGGTTCGTCAGCGCGGGAGCAGCAGGTATTAACATAACAGGCCGATC 1263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1012 CATACCTTCAAGGTTGTCCTAGCGAGGAGCTCGACTTACAACCTTCGTCATCCGTT 1071

QY 1364 TTCGCGACGTCGTCGAGCAGCGGCACGCCCGCGGGCGACAACGTCACGATCCGTTTC 1323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1072 GAGCGAGATGTTGTCACAGTTGG-----TCAAGCTGGCGACATGTCACCATTCGATTC 1125

QY 1324 CAGACGACCAACCCCGGCGCGCTGTTCTCTCCATGTC 1359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1126 GTCCTGATATGCTGCTCCCTGGATTCTTCACTGC 1161

RESULT 13
US-09-181-827A-22
; Sequence 22, Application US/09181827A
; Patent No. 6242232
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberly M.
; APPLICANT: Kaupinen, Sakari
; APPLICANT: Hakler, Torben P.
; TITLE OF INVENTION: Purified Coprinus Laccases And Nucleic
; FILE REFERENCE: 4554.200-US
; CURRENT APPLICATION NUMBER: US/09/181.827A
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/002.800
; PRIOR FILING DATE: 1995-08-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Coprinus cinereus
US-09-181-827A-22
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Query Match 29.3%; Score 439.6; DB 4; Length 1161;
Best Local Similarity 63.4%; Pred. No. 1.3e-89;
Matches 746; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

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QY 190 CACTGGCAGCGTTCTTCAGCAGGACCAACTGGGCGAGGAGGACCGCGCTTGGTCAAC 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CACTGGCAGCGTTCTTCAGGAGGAGGTACAGCTTGGCGCGAGCGTCTCGGGTGTACT 60

QY 250 CAGTGCCTATTGCTTCGGGCAATTCATTTCTGTACGACTTCCATGTGCCCGACAGCA 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CAATGCCCATTTGCCCTTGGTCACTCTTCTCTATAAGTTCCAGGCCAAAACCAAGCT 120

QY 310 GGAAGCTTCTGGTACCACAGTCATCTGTCTAGCAATCTGTGACGGGTGCGAGGACCG 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GGTACTCTGTGTACCAATCCACACATGCTCTAGTATTGTGACGGCTGAGAGCGTC 180

QY 370 TTCGTGCTAGCAGCCCAAGGATCCGACGCCAGCGGTACGATGTGACAAACGAGGC 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATGGTGGCTTTACGATCCCTTAGATCCCATCTCTTCTCTATAAGTTCCAGGCCAAAACCAAGAT 240

QY 430 AGGGTGCATCAGCTTGACCGACTGTACCAACCGCTGCCCGGCTCGGTCCCAAGTCCCA 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACTATCATCAGCTCGCGACTGGTATACGATCCGAGGCGGTTTACCCAGGCGGACCGTCGTC 300

QY 490 CTCGGCGCGAGCGCCACGCTCATCAATGTCTTTGGCGGCTCGGCTCCACTCCCAACCGCC 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ACCCCCTGG---TCGACTTTGATCAATGCAAGGCGGTTTACCCAGGCGGACCGTCGTC 357

QY 550 GGGCTTGTGTGATCAAGTCCAGCAGCAAGAGCGGTACCGCTTCGGTCTCGTTTCGATC 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 CCCTTGGCGCTGATTACAGCTCAGCGCGGGAAGCGCTACCGCTTCGGCTCGTCTCCCTT 417
```


Qy	610	TCGTGCGACCCGAACCTACAGGTTACCACTGACGAGGCGACAATCTGACCGTCATCGAGGTC	669
Db	418	TCGTGCGACCCGAACCTACAGGTTACCACTGATTTCTCTATTGACGGTCACACCATGACGGTCAATTGAAGTC	477
Qy	670	GACGGGTATCAACGACGAGCCTCTCCTTTGTTCGACTCTATCCAGATCTTCGCGCGCAGCGC	729
Db	478	GATGGTCAACCATGAACCGTTGGTTGTCGACCAATCAATCTTTGCTGGTCAACGG	537
Qy	730	TACTCTTTGTGTGTAATCGGAACCAACGGTCGGCAACTACTGGGTCCGCGCAACCCG	789
Db	538	TACTCGTTGTCTTTGAACCCCAACGCGCGCTCAACAACCTACTGGGTCAAGGCTAAACCC	597
Qy	790	AACCTTCGGAACGGTTGGTTTCGCGGGGGATCAACTCGGCATCTCGCGCTACCAAGGC	845
Db	598	AACCTCGGCTCTCTCGGCTTCGGTGGCGGTATTAAATTCGCAATTCCTCGATATGTTGGA	657
Qy	850	GCACCACTGCGCGAGCCCCACTACGACCCAGACGAGTCGGTGATCCCGCTTTATCGAGACG	909
Db	658	GCTCTCGGCTCGACCCCAACCACTCCCAATTTGCCCTTTACGCAACCCACTCCTCGAGACC	717
Qy	910	AACCTGCACCCCTCGCTCGCATGCTGTGCTGTGCGCGCCGACACACCGGGGGGTGACG	969
Db	718	AACCTGCACCCCTCTGTAATCTGTCGACCTGCGCGCCCTCCCGCGGTGACGTCGAT	777
Qy	970	AAGCGGCTCAACCTCGCGTTTAACTTCAACGGCAC-----CAACTCTTCTCATCAACAAC	1023
Db	778	GTGCGCATCAACCTGGATATCTGTTTCGAGCTCTCAATCCTCAAGTTCACCTGTCACGGT	837
Qy	1024	GCACATTTACGGCGCGGACCGTCCGGGTACCTCTCCAGATTTCTGAGCGGTGCGCAGACC	1083
Db	838	GCTACCTTCGATGAACACACCCGTTCCGGTCCCTCTCCAGATTTTGAGCGGTGCACATACC	897
Qy	1084	GCACAAGACCTGCTCCCTTCAGGCTCTGCTACCGGCTCCCGGCCACTCCACCATCGAG	1143
Db	898	GCCTCATCTCTCTCCCTCTGGCAGGCTACACTCTTCCCTTAAACAGGTCAATTGAG	957
Qy	1144	ATCACGCTGCCGCGACCGCTTTGGCCCCGGGTGACGCGACCCCTTCACCTCGACGGT	1203
Db	958	CTCACTATTCCCCGTGGTGGTAT-----CGGTGCTCTCACCCCATCATCTTACAGGC	1011
Qy	1204	CACGCTTCGCGGTCTTCGACGCGGGGACCAACCGTATTAAGTACAGCAGCCGATC	1263
Db	1012	CATACCTTTCAAGTTGTTCGCTAGCGACGAGCTCGACTTACAACCTCGTCAATCCCGGT	1071
Qy	1264	TTCCGGGAGCTGCTGAGCAGGCGCACGCGCGCGGGGCGACAGCTCAGCATCGGTTTC	1323
Db	1072	GAGCGAGATGTTGTCAACGTTGG-----TCAAGCTGGCGACATGTCCACATTCGATTTC	1125
Qy	1324	CAGAGGACAAACCCCGGGCGGTGTTCTCTCACTGC	1359
Db	1126	GTCACTGATAAATGCTGGTCCCTGGATTCTTCACTGC	1161

RESULT 14

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US-08-689-421-18
: Sequence 1F, Application US/08689421
: Patent No. 6008029
:
: GENERAL INFORMATION:
:
: APPLICANT: Yaver, Debbie S.
: APPLICANT: Brown, Kimberley M.
: APPLICANT: Kauppinen, Sakari
: APPLICANT: Halkier, Torben P
: TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
: TITLE OF INVENTION: ENCODING SAME
:
: NUMBER OF SEQUENCES: 36
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: No. 6008029o No. 6008029disk of No. 6008029th America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
:
: CITY: New York
:
: STATE: New York
:
: COUNTRY: United States of America
:
: ZIP: 10174-6401
:

```

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598 AACAGGGTCGAAACGGAGCTTGGTGTACCTTCGCAACGGTGTCAACTCGGCCATCCTT 657
838 CGCTACCAAGCGGCACCAAGTCCGCGAGCCCACTAGCAGCCAGAGCGTTCGGTATCCCG 897
658 CGCTATCGCGCGGTGCAACGCTGATCAACACCTCCGCAACCCCAACCCGCGCCAA 717
898 CTTATCGAGAGAACTTCACCCCTCCCTCGCATGCTGTGCTGCGAGCCGACACCC 957
718 CTCAGGAAGCGGACCTCCATGCTCATCGACCCGCTGCTCCGGTATCCCACTCCG 777
958 GGGGCGCTCGACAGGCGCTCAACTCGCGTTTAACTTCAACGGCAGCAAACTTCTTCATC 1017
778 GCGCTGCAGAGCTCAACCTCCGATTCCAATTGGGCTTCAGCGCGGTTCAGGATT 837
1018 AACACGCGACTTTCACGCGCGGACGCTCCGCGGTACTCTCCAGATTCTGAGCGGTGCG 1077
838 AACGGAACCGGATAGAGAGTCCAAAGCTTCTTACGCTTTCGAGATTATGAGTGGTGG 897
1078 CAGACCGCACAGAGCTCTCCCTGCAAGCTCTGTCTACCGGCTCCCGGCCACTCCAC 1137
898 CAGAGTGGAAAGCACTTCTCCCTGCTGATCGGTGTATGATTGCC-----CAGGAAC 951
1138 ATCGAGATCAGCTGCCGCGACCGCTTGGCGCGGGGTGCGACCGCACTTACATACAC 1197
952 CAAGTTGTTGAGCTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
1198 CACGCTCAGCGCTTCGCGGTGCTTTCGACGCGGGGAGCAGCAGCTATACATACAC 1257
1012 CACGCTATGCGTTCAGTGTGCTCAGGAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1071
1258 CCGATCTTCCGCGAGCTGCTGAGCAGCGGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 1317
1072 CCGGTCAGCGCGATGTTGTTAGTCTGG-----TGTTACTGGAGAGAAATTACCA 1125
1318 CGCTTCCAGAGCGAACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1367
1126 CGATTGCTCAGCGATAACCGAGCGCGCGGTGTTCTTCCACTGCCACATTGA 1175
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RESULT 15

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US-09-389-528-18
; Sequence 18, Application US/09389528
; Patent No. 6207430
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6207430o No. 6207430disk of No. 6207430th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,528
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,421
; FILING DATE: 9-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
```

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; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4554.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1176
; US-09-389-528-18

Query Match 25.2%; Score 377.6; DB 4; Length 1176;
Best Local Similarity 60.0%; Pred. No. 9.2e-76;
Matches 714; Conservative 0; Mismatches 449; Indels 27; Gaps 4;

Qy 190 CACTGGCAGCGCTTCTCCAGGCAGGCACCACTGGGCGAGGACGCGCGTTCGTCAC 249
Db 1 CATTGGCAGCGTCTCTCCAAAGGGGACCAACTGGGCTGATGGTGCAGATGGTGTCAAC 60
Qy 250 CAGTGCCCTATTGCTTCCGGGCATTCTTCTGTACGACTTCCATGTGCCGACCAAGCA 309
Db 61 CAGTGCCGATCTCTCCAGGCCATGCTTCTCTACAGTTCACTCCAGCTGGCCACGCT 120
Qy 310 GGAAGTTTCTGGTACCAAGTCACTGTCTACGCAATCTGTGACGGGCTGCGAGGACG 369
Db 121 GGTACTTTCTGGTACCACTTCCACTTTGGCACCACCAATCTGCGATGGTCTCGTGGTCCA 180
Qy 370 TTCGTCGTTAGCAGCCCAAGATCCGACGCGCCAGCCCTAGGATGTTGACAAACAGAGC 429
Db 191 ATGGTCATTACGAGCAGACATGACCCACAGCTGCGCTCTACGAGAGATGACGAGAAC 240
Qy 430 ACGGTTCATCAGTTGACCGACTGTTACACACCGCTGCCCGCTCGGTCCAGGTTCCCA 489
Db 241 ACCATCATTAAGCTTCCGCGATTGGTACCATATCCCGCTCCCTCCATTC---AGGTTGCT 297
Qy 490 CTCGGCGGAGCGCACGCTCATCAATGTTTGGGCGGTGCGGCTCCACTCCCAACCGCC 549
Db 298 GCCAGCTGACGCTACGCTCATCAACGTTAGGTGCTGCTAGTGGGCGGCGCCAGCTGCC 357
Qy 550 GCGTTTGTGTGATCAACGTCAGCAGCAAGGCGCTACCGCTTCGCTTCGTTTCGATC 609
Db 358 GAGCTTTCGATCGTCAATGTCGAGCAAGGAAGTAGTACCGAATGCGTTTGTATCTCGTG 417
Qy 610 TCGTGGACCGGAACTACAGTTTACGATCGAGGCGACAACTGACCGTCAATCGAGGTC 669
Db 418 TCCTCGGACCGCAACTGGCAGTTCTCCATTGACGAGCATGAGTTGACGATCATTTGAAGTC 477
Qy 670 GACGGTATCAACAGCCAGCTCTCTTCTCGACTTATCCAGATCTTCCGCGCGAGGCG 729
Db 478 GATGTCAGCTACTGAGCGCGCATACGTTGATGCTCTCCAGATCTTCTACTGGTCAAGG 537
Qy 730 TACTCTTTGTGTTGAATGCGAACAACCGTCGCGCAACTACTTGGTTCGCGCGAACCGG 789
Db 538 TACTCTTTCGTTCTCGAGCGCAACCGCGGTGGGACAACTACTGATCGTGTCAACCC 597
Qy 790 AACTTCGGA-----ACGGTTGGTTTCGCGGGGAGATCACTTCGCCATCTCTG 837
Db 598 AACAGGGTCGAAACGGAGCTTGGTGTACCTTCGTCACCGAGGTTGTCACCTCGGCCATCT 657
Qy 838 CGCTACCAAGGCGCAGCTGCGGAGCCCACTACGAGCCAGACCGCTCGGTGATCCCG 897
Db 658 CGCTATCGCGCGCTGCGCAACGCTGATCAACACCTCCGCAACCCCAACCCGCGCCAA 717
Qy 898 CTTATCGAGAGAACTTTCACCCCTCCCTCGCATGCTGTGCTGCGAGCGCGCGACACCC 957
Db 718 CTCAGAGCGGAGCTCTCATCGACCCGCTGCTCCCGGTATCCCACTCCG 777
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QY 958 GGGGGGCTGCACAAGGGCGCTCAACCTGCGGCTTTAACTTCAACGGCACCACCAACTTCTTCATC 1017
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Db 778 GGGGCTGCAGACGTCACACCTCCGATTCCAAATTGGGCTTTCAGCGGTCGATTACAGATT 837
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QY 1018 AACACGCGACTTTCAGCGCGCGACCGTCCCGGTACTCCTCCAGATTCTGAGCGGTGCG 1077
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 AACGGAACCGCATACGAGAGTCCAAAGCTTCCTACGCTCTTGAGATTATGAGTGTGCG 897
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QY 1078 CAGACGCGCACAGACCTGCTCCCTGACGGCTCTGTCTACCCGCTCCCGGCCACTCCACC 1137
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 CAGAGTGCAGAACGACTTGCTCCCTGCTGGATCGGTGTATGAGTTGCC-----CAGGAAC 951
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1138 ATCGAGATCACGCTGCCCGGACCGCTTGGCCCGGGTGACCGACCCCTTCCACCTG 1197
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 CAAAGTTGTTGAGCTTGTGTCTGCTGTGTTCTCGGTGCTCCTCGGTGCTCATCCTTTCCATCTC 1011
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1198 CACGGTCACGCCCTTCGCGGTCGTTGCGAGCGCGGGAGCACACGTTATAACTACAAGAC 1257
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 CACGGTCATGCGTTCAGTGTGTCAGAGTGTCAGGAGTGACAGGACGACACCTACAACCTTGTCAAC 1071
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1258 CCGATCTTCGGCAGCTGCTGTAGCACGGGCACGCCCGCGCGGGCGACACACGTCACGATC 1317
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1072 CCGGTCAAGCGCGATGTTGTTAGTCTTGG-----TGTTACTGGAGACGAAGTTACCAT 1125
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1318 CGCTTCCAGACGACACACCCCGCGGCTGTTCTCCTCAGTGCACATCGA 1367
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1126 CGATTCGTACCGATAAACCAGCGCGTGTCTTCCACTGCGCACATTGA 1175
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: December 14, 2002, 05:21:02
Job time : 103 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 08:22:47 ; Search time 45 Seconds
(without alignments)
1066.024 Million cell updates/sec

Title: US-09-786-960-2
Perfect score: 2669
Sequence: 1 AIGPVASLVVANAPVSPDGF.....VPKAWSLCPIYDGLSEANQ 499

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	2243	84.0	520	2	A35883	laccase (EC 1.10.3
2	2238	83.9	520	2	B35883	ligninolytic pheno
3	1917.5	71.8	527	2	JC5357	laccase (EC 1.10.3
4	1882.5	70.5	520	2	S59533	laccase (EC 1.10.3
5	1871.5	70.1	520	2	JC5356	laccase (EC 1.10.3
6	1772	66.4	512	2	JC5355	laccase (EC 1.10.3
7	1743.5	65.3	529	2	S49120	laccase (EC 1.10.3
8	1743.5	65.3	533	2	S62371	laccase (EC 1.10.3
9	1716	64.3	548	2	S18746	laccase (EC 1.10.3
10	1175.5	44.0	529	2	S68120	laccase (EC 1.10.3
11	1000	37.5	599	2	S68118	laccase (EC 1.10.3
12	930.5	34.9	572	2	S68119	laccase (EC 1.10.3
13	901	33.8	576	2	S68117	laccase (EC 1.10.3
14	622.5	23.3	621	2	S72493	laccase (EC 1.10.3
15	608	22.8	624	2	A36962	laccase (EC 1.10.3
16	601.5	22.5	619	1	KSNCL0	laccase (EC 1.10.3
17	600.5	22.5	619	1	KSNCLT	laccase (EC 1.10.3
18	599	22.4	636	2	AS5428	ferroxidase precu
19	597.5	22.4	622	2	S56214	probable membrane
20	574.5	21.5	582	2	T05020	L-ascorbate oxidas
21	567	21.2	553	2	T45959	laccase-like prote
22	566	21.2	555	2	T48347	laccase-like prote
23	556	20.8	622	2	S62580	probable multicopp
24	538.5	20.2	557	2	JC5229	laccase (EC 1.10.3
25	536.5	20.1	587	1	KSKVA0	L-ascorbate oxidas
26	535.5	20.1	567	2	T44928	L-ascorbate oxidas
27	530.5	19.9	578	2	S66353	L-ascorbate oxidas
28	530	19.9	554	2	T01240	laccase (EC 1.10.3
29	524.5	19.7	570	2	T00579	probable laccase [

30 516.5 19.4 573 2 T02743 laccase (EC 1.10.3

31 514.5 19.3 551 2 T02752 probable laccase (

32 510 19.1 552 2 A51027 L-ascorbate oxidas

33 497 18.6 579 2 S11027 L-ascorbate oxidas

34 494.5 18.5 569 2 E84904 probable laccase (

35 493 18.5 569 2 T48484 laccase-like prote

36 487.5 18.3 576 2 E86316 protein T10022.11

37 484.5 18.2 584 2 T45944 laccase-like prote

38 478 17.9 580 2 F84828 probable laccase (

39 465 17.4 586 2 T45945 laccase-like prote

40 395.5 14.8 380 2 T04343 L-ascorbate oxidas

41 392 14.7 608 2 S69564 hypothetical prote

42 381 14.3 713 2 T21201 hypothetical prote

43 371 13.9 409 2 T03788 laccase (EC 1.10.3

44 365 13.7 504 2 F70813 hypothetical prote

45 355 13.3 570 2 H87368 copper-binding pro

ALIGNMENTS

RESULT 1

A35883

laccase (EC 1.10.3.2) A - white-rot fungus (Trametes versicolor)

N:Alternate names: ligninolytic phenoloxidase 1 precursor

C:Species: Trametes versicolor (white-rot fungus)

C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 19-May-2000

C:Accession: A35883; S59526

R:Kojima, Y.; Tsukuda, Y.; Kawai, Y.; Tsukamoto, A.; Sugiura, J.; Sakano, M.; Kita, J. Biol. Chem. 265, 15224-15230, 1990

A:Title: Cloning, sequence analysis, and expression of ligninolytic phenoloxidase gene from the white-rot fungus Trametes versicolor

A:Reference number: A35883; MUID:90368706; PMID:2394718

A:Accession: A35883

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-520 <KOJ>

A:Cross-references: GB:M60560; GB:J05562; NID:g167464; PIDN:AAA33103.1; PID:g167465

R:Joenson, L.; Sjoestrom, K.; Haegstroem, I.; Nyman, P.O. Biochim. Biophys. Acta 1251, 210-215, 1995

A:Title: Characterization of a laccase gene from the white-rot fungus Trametes versicolor

A:Reference number: S59526; MUID:95399443; PMID:7669813

A:Accession: S59526

A>Status: preliminary

A:Molecule type: protein

A:Residues: 351-360 <JOE>

C:Superfamily: laccase

C:Keywords: oxidoreductase

Query Match 84.0%; Score 2243; DB 2; Length 520;

Best Local Similarity 81.8%; Pred. No. 1.6e-157;

Matches 408; Conservative 35; Mismatches 56; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGFRLDAIVVGVVPSPLITGKGRFQNLNVVDLTNHSMLKS 60

Db 22 AIGPTADLLTISNAEVSFDGFARQAVVNVNTPGLVAGNKGDRFQNLNLTNHSMLKS 81

QY 61 TSIHWGFTQAGPNWADGPAFVNVQCPISAGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120

Db 82 TSIHWGFTQAGPNWADGPAFVNVQCPISAGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 141

QY 121 RGFVYVDPKDPHASRYDVNDSTVTLTDWYHTAARLGRPRFPLGADATLNLGLRSAST 180

Db 142 RGFVYVDPNDPASHLYDVNDSTVTLTDWYHTAARLGRPRFPLGADATLNLGLRSAST 201

QY 181 PTAALAVINVQHGKRYRFRFLVLSICDPNTFTSIDGHNLTAVIEVDGNSQPLLVDSIQIFA 240

Db 202 TAADLAVINVTKGRYRFRFLVLSICDPNHTFTSIDGHDLTAVIEVDGNSQPLLVDSIQIFA 261

QY 241 AQRYSFLVLANQTVGVNWRANPNFTGVFAGGINSAILRYQCAPVAEPTTTQTTSTVIPL 300

Db 262 AQRYSFLVLANQTVGVNWRANPNFTGVFAGGINSAILRYQCAPVAEPTTTQTTSTVIPL 321

QY 301 IETNLHPLARMVPVSGSPTPGGVDKALNLAFAFNFGTNNFTTPTTPTVPLQLLSGAQ 360

Db 322 NEVDLHPLATMAVPGSVAGVDTAIINAFNNGTNGFFINGASFVPTVPVLLQIISGAQ 381
Qy 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPAGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPHLLHGHAFVAVRSAGSTTYNDP 441
Qy 421 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
Db 442 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 501
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 502 PKAWSDLCPYDGLDVNDQ 520

RESULT 2
B35883
ligninolytic phenoloxidase (EC 1.10.1.1) 2 precursor - white-rot fungus (Trametes versicolor)
C:Species: Trametes versicolor (white-rot fungus)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 19-May-2000
C:Accession: B35883
R:Kojima, Y.; Tsukuda, Y.; Kawai, Y.; Tsukamoto, A.; Sugura, J.; Sakano, M.; Kita, Y.
J. Biol. Chem. 265, 15224-15230, 1990
A:Title: Cloning, sequence analysis, and expression of ligninolytic phenoloxidase genes
A:Reference number: A35883; MUID:90368706; PMID:2394718
A:Accession: B35883
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-520 <KOJ>
A:Cross-references: GB:J05562
C:Superfamily: laccase
C:Keywords: Oxidoreductase

Query Match 83.98; Score 2238; DB 2; Length 520;
Best Local Similarity 81.68; Pred. No. 3.6e-157;
Matches 407; Conservative 35; Mismatches 57; Indels 0; Gaps 0;
Qy 1 AIGPVASLVANAPVSPDGLRDAIVNVGVVPSPLITGKGRFQNLNVDPLTNHSLMS 60
Db 22 AIGPTADLTISNAEVSPPGFAQVAVVNVVTPGVLVAGKGRFQNLNVDPLTNHSLMS 81
Qy 61 TSIHHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 82 TSIHHGFFQAGTNWADGPAFVNOCPISGHSFLYDFQVPDQAGTFWYHSHLSQYCDGL 141
Qy 121 RGPVVVYDPPKPHASRYDNDNESTVITLTDWYHTAARLGRFPPLGADATLNGLSRST 180
Db 142 RGPVVVYDPPKPHASRYDNDNESTVITLTDWYHTAARLGRFPPLGADATLNGLSRST 201
Qy 181 PTAALAVINVQHKRYRFLVSIQDNPYTFSGIDGHNLTIVEDGINSOPLVDSIQIFA 240
Db 202 TPAALAVINVQHKRYRFLVSIQDNPYTFSGIDGHNLTIVEDGINSOPLVDSIQIFA 261
Qy 241 AQRYSFVLNANOTVGNVWRANPNFTGPGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 300
Db 262 AQRYSFVLNANOTVGNVWRANPNFTGPGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 321
Qy 301 IETNLHPLARMVPVPGSPPTGGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 360
Db 322 NEVDLHPLATMAVPGSVAGVDTAIINAFNNGTNGFFINGASFVPTVPVLLQIISGAQ 381
Qy 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPAGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPHLLHGHAFVAVRSAGSTTYNDP 441
Qy 421 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
Db 442 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 501
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 502 PKAWSDLCPYDGLDVNDQ 520

RESULT 3
JC5357
laccase (EC 1.10.3.2) 5 precursor - white-rot fungus (Trametes villosa)
N:Alternate names: urushiol oxidase
C:Species: Trametes villosa (white-rot basidiomycete)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: JC5357
R:Taver, D.S.; Gollightly, E.J.
Gene 181, 95-102, 1996
A:Title: Cloning and characterization of three laccase genes from the white-rot basid
A:Reference number: JC5355; MUID:97128774; PMID:8973314
A:Accession: JC5357
A:Molecule type: DNA
A:Residues: 1-527 <YAV>
A:Cross-references: GB:I78078
C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phen
C:Keywords: pathogenesis.
C:Genetics:
A:Gene: lcc5
A:Introns: 63/3; 86/3; 127/1; 165/1; 186/2; 220/2; 272/3; 357/3; 431/3; 470/3; 509/3
C:Superfamily: laccase
C:Keywords: oxidoreductase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-527/Product: laccase 5 #status predicted <MAT>
Query Match 71.8%; Score 1917.5; DB 2; Length 527;
Best Local Similarity 70.5%; Pred. No. 1.6e-133;
Matches 356; Conservative 47; Mismatches 93; Indels 9; Gaps 3;
Qy 1 AIGPVASLVANAPVSPDGLRDAIVNVGVVPSPLITGKGRFQNLNVDPLTNHSLMS 60
Db 24 AIGPTADLTISNAEVSPPGFAQVAVVNVVTPGVLVAGKGRFQNLNVDPLTNHSLMS 83
Qy 61 TSIHHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 82 TSIHHGFFQAGTNWADGPAFVNOCPISGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 143
Qy 121 RGPVVVYDPPKPHASRYDNDNESTVITLTDWYHTAARLGRFPPLGADATLNGLSRST 180
Db 144 RGPVVVYDPPKPHASRYDNDNESTVITLTDWYHTAARLGRFPPLGADATLNGLSRST 203
Qy 181 PTAALAVINVQHKRYRFLVSIQDNPYTFSGIDGHNLTIVEDGINSOPLVDSIQIFA 238
Db 204 GGGATNLTVITVQGRYRFLVSIQDNPYTFSGIDGHNLTIVEDGINSOPLVDSIQIFA 263
Qy 239 FAQRYSFVLNANOTVGNVWRANPNFTGPGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 298
Db 264 FAQRYSFVLNANOTVGNVWRANPNFTGPGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 323
Qy 299 PLIETNLHPLARMVPVPGSPPTGGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 358
Db 324 PLIETNLHPLARMVPVPGSPPTGGVDKALNLAFFNGTNNATFTPTTPTTQTSVI 383
Qy 359 AQTADLLPAGSVYPLPAHSTIETLPTALAPAGAPHPHLLHGHAFVAVRSAGST 413
Db 384 AQTADLLPAGSVYPLPAHSTIETLPTALAPAGAPHPHLLHGHAFVAVRSAGST 443
Qy 414 TYNNDPLFRDVGSTGTPTAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVAD 473
Db 444 TYNNDPLFRDVGSTGTPTAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIYFAEDVAD 501
Qy 474 VKAANPVKAWSDLCPYDGLSEAN 498
Db 502 TASANPVTAWSDLCPYDGLDSSD 526

RESULT 4
S59533
laccase (EC 1.10.3.2) precursor - white-rot fungus (Trametes versicolor)
C:Species: Trametes versicolor (white-rot fungus)
C:Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 19-May-2000

pathogenesis.
C:Gene: lcc4
A:Gene: lcc4
C:Introns: 62/3; 85/3; 126/1; 185/2; 217/2; 269/3; 335/3; 424/3; 463/3; 503/1
C:Superfamily: laccase
C:Keywords: oxidoreductase
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-520/Product: laccase 4 #status predicted <MAT>

Query Match 70.1%; Score 1871.5; DB 2; Length 520;
Best Local Similarity 68.5%; Pred. No. 3.8e-130;
Matches 342; Conservative 57; Mismatches 97; Indels 3; Gaps 2;

Qy 1 AIGPVASLVVANAPVSDGFELDRDAIVNVGVPSPLITGKGGDRPQLNVDTLTNHSMKS 60
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 23 AIGVTELTISNGDVPDGETRAAVLANGVFPGLITGNKGDNFIQINIDLSNETMLKS 82
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 61 TSIWHGFFOAGTNNADGPFAFVNOCPTASGHSRLYDFHFVDPDOAGTFWYHSHLSTQYCDGL 120
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 83 TSIWHGFFOAGTNNADGAFAFVNOCPIATGNSFLYDTFTADQAGTFWYHSHLSTQYCDGL 142
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 121 RGPVVYVDPKDPHASRYDVONESTVITLTDMYTAAALRGPRFLGADATLINGLRSAST 180
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 143 RGPVVYVDPSPDHADLYDVDDETTIITLSDWYHTAASLGAAFPDGSDSTLINGLRFAGG 202
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 181 PTAALAVINVQHGRYRFRFLVSICDDNYFSDIGHNLTVIEVDGINSQPILLVDSIOIFA 240
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 203 DSTDLAVITVEQGKRYSRMRLSLSCDPNYFSDIGHNMNTIEADVAVNEHLTVDSIQIYA 262
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 241 AQRSFVLNANOTVCNTVWRANPNFGVGFAGGINSAILRYQGAPVAEPETTOTTTSVIPL 300
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 263 GORYSFVLTDADDIDNFIRALPSAGTISDGGINSAILRYSGASEVDPTTTTSTVLPL 322
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 301 IETNLHLPMVPVGSTPGGVSKALMALNFNGTNEFINNATFTPTTPVPLLQLSQAQ 360
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 323 DEANLVPLDSPAAPGDPNIGVDYVALNDFNFDGTNEFFINDVSFVSPVLPVLLQLSGTT 382
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 361 TAQDLLPAGSVYPLPAHSTTEITLPAATAL-APGAPHFHLGHAFVVRSGASTTYNYND 419
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 383 SAADLLPSGSLFAYVPSNSTEISPITATNACGAPHPFHLLGHTFSIVRTAGSTDNTFVN 442
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 420 PIFRDVYSTGTPAAGDNVTIRFQDNPMPWLHCHIDFHLADAGFAIYFAEDADVKAANP 479
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Db 443 PVREDVYNTGT--VGDNVNTRFTDNPDPWFLHCHIDFHLAEAGFAIYFSEDADVSNITT 500
||||| :|| ||||||| :|| | ||||| ||||| :|| :|| :||
Qy 480 VPKAWSDLCPITYDGLSEAN 498
||||| :|| :||
Db 501 PSTAWEDLCPTYNALDSSD 519
||||| :|| :||

RESULT 6
JC5355
laccase (EC 1.10.3.2) 3 precursor - white-rot fungus (*Trametes villosa*)
N:Alternate names: Urushiol oxidase
C:Species: *Trametes villosa* (white-rot basidiomycete)
C>Date: 28-May-1997 #sequence_revision 28-May-1997 #text_change 19-May-2000
C:Accession: JC5355
R:Yaver, D.S.; Golightly, E.J.
Gene 181, 95-102, 1996
A:Title: Cloning and characterization of three laccase genes from the white-rot basid
A:Reference number: JC5355; MUID:97128774; PMID:8973314
A:Accession: JC5355
A:Molecule type: DNA
A:Residues: 1-512 <YAV>
A:Cross-references: GB:I78076
C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phen
pathogenisis.
C:Genetics:
A:Gene: lcc3
A:Introns: 61/3; 84/3; 125/1; 163/1; 184/2; 211/2; 263/3; 330/3; 349/3; 416/3; 455/3;
C:Superfamily: laccase
C:Keywords: oxidoreductase
F:1-21/Domain: signal sequence #status predicted <SIG>

F;22-512/Product: laccase 3 #status predicted <MAT>

Query Match 66.4%; Score 1772; DB 2; Length 512;
Best Local Similarity 67.5%; Pred. No. 8e-123;
Matches 333; Conservative 38; Mismatches 112; Indels 10; Gaps 4;

QY 1 AIGPVASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGRFQNLNVDTLTNHSMLKS 60
DB 22 SIGPVTELDIVNKVIADPGVARDIVLAGGTFPGPLITGKGRDNFRINVDKLVNQTMLS 81

QY 61 TSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
DB 82 TTIHHGFMQHTTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 141

QY 121 RGPVFWDPKPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADATLNGRST 180
DB 142 RGPLVYDHPDQAYLIDVDDESVITLTDWYHTAARLGPREFLGADATLNGRST 196

QY 181 PTAALAVINVOGKRYRFLRYSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 197 PTADLAVIEVQHKRYRFLRYSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQIFA 256

QY 241 AQRYSFVLNANQTVGNVWRANPN-FGTVGFAAGINSAILRYQCAPVAEPTTOTTVIP 299
DB 257 AQRYSFVLNANQTVGNVWRANPN-FGTVGFAAGINSAILRYQCAPVAEPTTOTTVIP 316

QY 300 LIETNLHPLARMPVPGSPTPGGVDKALNLAFFNCTNFINNATFTPTVPVLLQILSGA 359
DB 317 LWETDLHLTPDPRAPGLPFKGGVDHALNLTFFNGSEFFINDAPVPTVPVLLQILNGT 376

QY 360 QTAQDLPLAGSYVPLPAHSTIEITLPATAPAGPHPLHGHAFVAVRSAGSTTYNYND 419
DB 377 LDANDLLPGSYVPLPAHSTIEITLPATAPAGPHPLHGHAFVAVRSAGSTTYNYND 434

QY 420 PIFRDVSTGTPAGDNVTIRFQDNPFWLHCHIDHPLDAGFAIYFAEDVADVKAANP 479
DB 435 PVKRTTVSIG--LAGDNVTIRFQDNPFWLHCHIDHPLDAGFAIYFAEDVADVKAANP 492

QY 480 VPKAWSDLCPYD 492
DB 493 VPEDNKNLCPTFD 505

RESULT 7
S49120
laccase (EC 1.10.3.2) precursor - oyster mushroom
N:Alternate names: diphenol oxidase
C:Species: Pleurotus ostreatus (Oyster mushroom)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 11-Jun-1999
C:Accession: S49120
R:Giardina, P.; Cannio, R.; Martirani, L.; Marzullo, L.; Palmieri, G.; Sannia, G.
A:Description: Gene structure of a phenol oxidase from the lignin degrading basidiomycet
A:Reference number: S49120
A:Accession: S49120
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-529 <GIA>
A:Cross-references: EMBL:Z34847; NID:G509380; PIDN:CAA84356.1; PID:G509381
C:Superfamily: laccase
C:Keywords: oxidoreductase

Query Match 65.3%; Score 1743.5; DB 2; Length 529;
Best Local Similarity 65.3%; Pred. No. 1.1e-120;
Matches 333; Conservative 53; Mismatches 105; Indels 19; Gaps 8;

QY 1 AIGPVASLVANAPVSPDGLRDAIV-----VNG---VPSPPLITGKGRFQNLNVDT 51
DB 24 AIGPTGDMYIVNEDVSPDGFTRSAVAVRSAPATDTPATATIPGVLVQGNKGNFQNLV 83

QY 52 LTNHSMKSTSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSH 111
DB 84 %SDTTMLKATSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSH 143

QY 112 LSTQYCDGLRGPFWVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADATLI 171
DB 144 LSTQYCDGLRGPFWVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADATLI 202

QY 172 NGIGRSASTPTAALAVINVOGKRYRFLRYSISCDPNYTFSDGHNLTVIEVDGINSQPL 231
DB 203 NGRGRFAGGTSALAVINVESNRYRFLRYSISCDPNYTFSDGHNLTVIEVDGINSQPL 262

QY 232 LVDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFAAGINSAILRYQCAPVAEPTT 291
DB 263 VDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFAAGINSAILRYQCAPVAEPTT 322

QY 292 TOTTSVPLIETNLHPLARMPVPGSPTPGGVDKALNLAFFNCTNF--FINNATFTPTPT 349
DB 323 TSSTST-PLEETNLVPLENPGAPVPGGADININLAMAFAVDVTFELTINGSPFKAPTA 381

QY 350 PVLLQILSGAQTADQLLPAGSYVPLPAHSTIEITLPATAPAGPHPLHGHAFVAVRS 409
DB 382 PVLLQILSGATTAASLLPSGSIYSLEANKVVEISIP--ALAVGGPHPLHGHAFVAVRS 439

QY 410 AGSTTYNNDPIFRDVTSTGTPAGDNVTIRFQDNPFWLHCHIDHPLDAGFAIYFAE 469
DB 440 AGSTTYNNDPIFRDVTSTGTPAGDNVTIRFQDNPFWLHCHIDHPLDAGFAIYFAE 498

QY 470 DVADVKAANPVPKAWSDLCPYDGLSEANQ 499
DB 499 DVTSTAP---PAAWDDLCPIYDALSDSK 525

RESULT 8
S62371
laccase (EC 1.10.3.2) precursor - oyster mushroom
C:Species: Pleurotus ostreatus (Oyster mushroom)
C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C:Accession: S62371; S62372; S49121; S54145
R:Giardina, P.; Aurilia, V.; Cannio, R.; Marzullo, L.; Amoresano, A.; Siciliano, R.;
Eur. J. Biochem. 235, 508-515, 1996
A:Title: The gene, protein and glycan structures of laccase from Pleurotus ostreatus.
A:Reference number: S62371; MUID:96184523; PMID:8654395
A:Accession: S62371
A:Molecule type: DNA
A:Residues: 1-533 <GIA>
A:Cross-references: EMBL:Z49075; NID:G785016; PIDN:CAA88895.1; PID:G785017
A:Accession: S62372
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-533 <GIZ>
A:Cross-references: EMBL:Z34848; NID:G785018; PIDN:CAA84357.1; PID:G785019
C:Genetics:
C:Introns: 46/2; 74/3; 97/3; 112/1; 128/2; 141/1; 160/2; 176/1; 185/3; 266/1; 274/1;
C:Superfamily: laccase
C:Keywords: glycoprotein; oxidoreductase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-533/Product: laccase #status predicted <MAT>
F:467/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 65.3%; Score 1743.5; DB 2; Length 533;
Best Local Similarity 64.8%; Pred. No. 1.1e-120;
Matches 330; Conservative 49; Mismatches 109; Indels 21; Gaps 7;

QY 1 AIGPVASLVANAPVSPDGLRDAIVNGV-----VPSPLITGKGRFQNLNV 49
DB 24 AIGPAGNYIVNEDVSPDGFTRSAVAVRSAPATDTPATATIPGVLVQGNKGNFQNLNV 83

QY 50 DTLTNHSMKSTSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYH 109
DB 84 NOLSDTTMLKATSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYH 143

QY 110 SHLSQYCDGLRGPFWVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADAT 169
DB 144 SHLSQYCDGLRGPFWVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADAT 202

Db 438 IVKSLGGTP-NYVNPVRDVRVG-----GTGVLRKTDNPGPWFVHCHIDWHLEAGLAL 492
Qy 466 VPAEDVAD-----VKANVPKAWSDLCPIYDGL 494
Db 493 VFAEAPSIROGVQSVQP-NNAWNOLCPKYAAL 524

RESULT 11
S68118
laccase (EC 1.10.3.2) 2 precursor [validated] - Rhizoctonia solani
C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pathogen
A:Reference number: S68117; MUID:96171523; PMID:8598061
A:Accession: S68118
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-599 <WAH>
A:Cross-references: EMBL:Z54276
A:Experimental source: strain RS22
C:Genetics:
A:Gene: lcc2
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 276/3; 408/3; 432/3; 469/2; 503/3; 555
C:Function:
A:Description: EC 1.10.3.2 [validated, MUID:96171523]
C:Superfamily: laccase
C:Keywords: copper; oxidoreductase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-599/Product: laccase 2 #status predicted <WAT>

Query Match 37.5%; Score 1000; DB 2; Length 599;
Best Local Similarity 38.7%; Pred. No. 7.5e-66;
Matches 226; Conservative 72; Mismatches 180; Indels 106; Gaps 14;

Qy 10 VANAPVSPDGLRDAIVNGVVPSPILITGKKGDRFQLNVDPLTTHNSLMKSTSIHWHGFF 69
Db 28 VANGAVAPDGVTRNAVLRNRPFGPLITANKGDTLKITVRNKLSDPTWRRSTIIHWHGLL 87
Qy 70 QAGTNWADGPAFVNPQCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPVYD 129
Db 88 QHRTAEEDGPAFVTCQPIPPQESYTYTMLPGTGTWYHSHLSQYDGLRGPVYD 147
Qy 130 KDPHASRYDVNDSVTITLTDWYHTAARLGRPRPLGA-----DATLINGLGR---- 176
Db 148 HDPYRNYDVEDERTVFTLADWYHT-----PSEAIATHDVLKTIIPDSGTINGKGYDPA 202
Qy 177 SASTPTAALA--VINQHGKRYRFLVSIQCDPNYTFSDIGHNLTVEVDGINSOPLIV 233
Db 203 SANTNNTTLENLYTLKVRGKRYRLINASAIASRFGVQGHKCTIIEADGLTKPIEV 262
Qy 234 DSITQIFAAQRYSFVLNANTVGNVWRA-----NPN----- 264
Db 263 DAFDILAGORYSCILKADQDPSYWINAPITNVLTNVQALLVYEDDKRPTHYPWKPFLT 322
Qy 265 -----PGTVGFAGGINSAT-----LRYQGAP 285
Db 323 WKISNEIIYQWQHKGSHGKHGHHKVRAGGVSGSLSRVSKRSASDLSKAVELAAAL 382
Qy 286 VA-----EPTTQTTSVIPLIETNLHPLARMPVPGSPPTGGVDKALNLAFFNNGTINFFIN 340
Db 383 VAGEAELDKRONEDNSTIVLDETCLIPVQPGAGGSRPADVVVPLDFCLNFANGLWTIN 442
Qy 341 NATFTPTTPVLLQILSGAQ--TAQDLLPAGSVYPLPAHSTTETITLPATALAPGAPHPH 398
Db 443 NVSYSPDPPTLLKILTDKDKVDASDFTADEHTYILPKNVVELHKGQAL--GIVHPLH 500
Qy 399 LHGHAFVVRSGSTTYNDPIFRDVRSTGTPAAGDNVTIRFQTDNPGPWFHCHIDPH 458
Db 501 LGHAFDVVQV-FGDNAPNTVNPVRDVR--GTYDAG--VRIQFRDNDPGPWFHCHIDWH 555

Qy 459 LDAGFAIVFAEDVADVKAANVPVK---AWSDLCPYDGLSEANQ 499
Db 556 LEEGFAMVFAEAPEDIKKSQSVKPDGQWKKCEKYEKLPEALQ 599

RESULT 12
S68119
laccase (EC 1.10.3.2) 3 precursor - Rhizoctonia solani
C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pathogen
A:Reference number: S68117; MUID:96171523; PMID:8598061
A:Accession: S68119
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-572 <WAH>
A:Cross-references: EMBL:Z54215; NID:g1150565; PIDN:CAA90942.1; PID:g1150566
A:Experimental source: strain RS22
C:Genetics:
A:Gene: lcc3
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 380/3; 404/3; 441/2; 476/3;
C:Superfamily: laccase
C:Keywords: copper; oxidoreductase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-572/Product: laccase 3 #status predicted <WAT>

Query Match 34.9%; Score 930.5; DB 2; Length 572;
Best Local Similarity 37.6%; Pred. No. 9.3e-61;
Matches 207; Conservative 68; Mismatches 206; Indels 69; Gaps 10;

Qy 7 SLVVANAPVSPDGLRDAIVNGVVPSPILITGKKGDRFQLNVDPLTTHNSLMKSTSIHWH 66
Db 25 NLKISNGKIADPGVTRNAVLRNRPFGPLITANKGDTLKITVRNKLSDPTWRRSTIIHWH 84
Qy 67 GFFQAGTNWADGPAFVNPQCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPVY 126
Db 85 GLLQHRNADDDGPAFVTCQPIPPQASYYTTPGLGDTGTWYHSHLSQYDGLRGLPLV 144
Qy 127 YDKDPHASRYDVNDSVTITLTDWYHTAAR-----LGRPFPLGADATLINGLGRSASTPT 182
Db 145 YDKDPHRRLLYDIDDEKTVLIIGDWYHTSSKAILATGNTITLQQPDSATINCKGRFPDPT 204
Qy 183 AA---LAVINVOHGKRYRFLVSIQCDPNYTFSDIGHNLTVEVDGINSOPLIV 238
Db 205 PANPNTLYTLKVRGKRYRLINASAIASRFGVQGHKCTIIEADGLTKPIEV 264
Qy 239 FAAQRYSFVLNANTVGNVWRA----- 261
Db 265 LAGRIDAVVEANQEPDITYWINAPLTNVANKTAQALLIVEDDRRYPHPKGPYRKWSYSE 324
Qy 262 -----NPNFGTVGFAGGINSAT-----LRYQAPVAPETTTQTTSVIPLIETNLHPLA 309
Db 325 ALIKYKWKHKGRLSGHGLKARMMEGSLHLHGRDRIVKRQNETTVV-MDETCLVPLE 383
Qy 310 RMPVPGSPPTGGVDKALNLAFFNNGTINFFINATFTPTTPVLLQILSGAQ--TAQDLLP 367
Db 384 HPGACAGCKPADLVLDLTFGVNFTTGHWMINGIPKHSKSPDMPPTLLKILTDGVTESDFTQ 443
Qy 368 AGSVYPLPAHSTTETITLPATALAPGAPHPHHLGHAFVVRSGAGSTTYNDPIFRDVVS 427
Db 444 PEHTIILPKNKCVFENIKGNS-GLGIVVHPILHLGHTFDVVO-FGNPNPNYVNPVRDVRV 501
Qy 428 TGTTPAAGDNVTIRFQTDNPGPWFHCHIDPHLDAGFAIVFAEDVADVKA--ANVPKAW 484
Db 502 ----ATDEGVRPQFQTDNPGPWFHCHIDWHLEEGFAMVFAEAPKGGPKSPVPRDQW 557
Qy 485 SDCPIYDGL 494
Db 558 KDLCKRYGSL 567

RESULT 13

S68117

laccase (EC 1.10.3.2) 1 precursor - Rhizoctonia solani

C:Species: Rhizoctonia solani

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 13-Mar-1998

C:Accession: S68117

R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollightly, E.J.; Halkier, T.; Kau

Curr. Genet. 25, 395-403, 1996

A:Title: The identification and characterization of four laccases from the plant pathogen

A:Reference number: S68117; MUID:96171523; PMID:8598061

A:Accession: S68117

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-576 <WAW>

A:Cross-references: EMBL:Z54275

A:Experimental source: strain RS22

C:Genetics:

A:Gene: lccl

A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 381/3; 405/3; 442/2; 477/3; 52

C:Superfamily: laccase

C:Keywords: copper; oxidoreductase

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-576/Product: laccase 1 #status predicted <MAT>

Query Match 33.8%; Score 901; DB 2; Length 576;
Best Local Similarity 37.7%; Pred. No. 1.4e-58;
Matches 212; Conservative 79; Mismatches 184; Indels 88; Gaps 18;

Qy 8 LVVANAPSPDGLRDAIVNGVSPSLITGKGRFQNLNVDTLTNHSMLKSTSIHHG 67

Db 26 LKISDGEIAPDGVKKNATLVNGYGPGLIFANKGTLKVKQNKLTNPENYRTTSIHHG 85

Qy 68 FQAGTNADGPAFYNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSTQYCDGLRPFVYV 127

Db 86 LQHRNADDGSPFTQCPVPRESYTYIPLDDQTGYWYHSHLSSQYVDGLRPLVIY 145

Qy 128 DPKDPHARSYVDNSTVITLTDWYHTAAR-----LGRPPLGADATLNGLSAST 180

Db 146 DPKDPHRLYVDDEKTVLLIGDWYHSSKAILASGNITRQPVSA---TINGKGRFDP 202

Qy 181 PTAA---LAVINVQHKRYRFLVSIISCDPNYTESIDGHNLTVEVGINSOPLVDSI 236

Db 203 NTPAMPDLYTLVKRGKRYRURVINSSEIASFVSFGHKVTVIAADGVSTKPYQVDAF 262

Qy 237 QIFAAQRYSFVLNANQTVGNWVRAN----PNFGTVGF-----AGGI 274

Db 263 DILAGORIDCVVEANQEPDTYINAPLTVNPKTAQALLVYEDRRPYHPKGPYKRSV 322

Qy 275 NSAILRYOG-----APVAEPT-----TTQTSVPIPLIETNLH 306

Db 323 SEAIKYNHKKHKGRLSGHGLKARMIEGSHHLSRSVVKRQNETTVV-MDESKLV 381

Qy 307 PLARMPVPGSPPG-GVDKALNLAFA--NFNGTNEFINNATPTPTVPVLLQILSCAQ--T 361

Db 382 PL---EYFGACGSPADLVLDLTFGLNATGCHWMINGIPYESKPIPTLLKILTEDGVT 438

Qy 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFLHGHAFAYVRSAGSTTYNYNDPI 421

Db 439 ESDFTKEETHVLPKNKCTEINKNSGIP-ITHPVHLGHGHWVYQ-FGNPNPNVNP 496

Qy 422 FRDVTSTGTPAAGDNVITRFQTDNPGPWFLHCHIDFHLDAAGFAIYFAEDADVKAANVP 481

Db 497 RRDVV--GSTDAG--VRIQFTDNPGPWFLHCHIDHLEEGFAMVFAEPAVKGG---p 549

Qy 482 KA-----WSDLCPIYDGLSEAN 498

Db 550 KSAVVDSSQWEGLCGYDNWLSN 572

RESULT 14

S72493

laccase (EC 1.10.3.2) precursor - Podospora anserina
N:Alternate names: benzenediol:oxygen oxidoreductase; urishiol oxidase
C:Species: Podospora anserina
C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C:Accession: S72493
R:Fernandez-Larrea, J.; Stahl, U.
Mol. Gen. Genet. 252, 539-551, 1996
A:Title: Isolation and characterization of a laccase gene from Podospora anserina.
A:Reference number: S72493; MUID:97071669; PMID:8914515
A:Accession: S72493
A:Molecule type: DNA
A:Residues: 1-621 <FER>
A:Cross-references: EMBL:Y08827; NID:g1729780; PIDN:CAA70061.1; PID:g1729781
A:Experimental source: strain ATCC 26003
C:Genetics:

A:Gene: lac2
A:Introns: 80/3; 111/1; 134/2
C:Function:
A:Description: catalyzes one-electron oxidation of mono-, di- and polyphenols, aminop
C:Superfamily: laccase
C:Keywords: copper; glycoprotein; oxidoreductase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-48/Domain: amino-terminal propeptide #status predicted <PRO>
F:49-605/Product: laccase #status predicted <MAT>
F:74-209/Domain: amino-terminal beta-barrel #status predicted <BB1>
F:210-366/Domain: middle beta-barrel #status predicted <BB2>
F:431-528/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F:606-621/Domain: carboxyl-terminal propeptide #status predicted <CRP>
F:133,261,276,289,325,334,382,401,421,441/Binding site: carbonyldehydrate (Asn) (covalent)
F:138,479/Binding site: copper (His) (type 2) #status predicted
F:140,183,185,481,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status p
F:476,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match 23.3%; Score 622.5; DB 2; Length 621;
Best Local Similarity 31.2%; Pred. No. 5.1e-38;
Matches 174; Conservative 71; Mismatches 184; Indels 139; Gaps 26;

Qy 15 VSPDGLRDAI-VVNGVVPSPILITGKGRFQNLNVDTLTNHSMLKSTSIHHGFFQAGT 73

Db 92 LGPDGVKQKVLNVDIFGPTITANWGDWIOVNNLRTN---GTSIHHGLRQKGT 147

Qy 74 NWADGPAFYNOCPISAGSHFLYDFHVPDQAGTFWYHSHLSTQYCDGLRPFVYVDPKDP 132

Db 148 NMHDGANGVTECPDPKGRSRIYRFA-QQYGTWYHSHFSAQYNGVGVTVIV---NGP 203

Qy 133 HASRYDQVNESTVITLTDWYHTAARL-----GPRPPLGADATLNGLSASTPTAA 184

Db 204 ASVPYDID--LGVPFITDYHKPADVLVEETMNGGPP---PSDTVLFKGHKNPQTGACK 258

Qy 185 LAVINVQHKRYRFLVSIISCDPNYTESIDGHNLTVEVGINSOPLVDSIQIFAAQRY 244

Db 259 FANVTLTPGKRHLRIINTSTHDFQLKLNHTMTIAADWVPVQAQTVDSLSFLAVGORY 318

Qy 245 SFVLNANQTVGNWVRANPNFCTVGFAGGI-----NSAILRYOGAPVAEPTTTOTT 295

Db 319 DVTIDANKSVGNWFNAT-----FGGLACGASLNPHPAAVFRIQAPNLTPLNIGT- 370

Qy 236 SVIPLIE-----TNLHPLARMPVPGS---PTPGVDVKALNLAFAFNENFTNFI----- 339

Db 371 ---PAADANCMDLNLTLPVWSRSVPTSGFTPRP---NNTLPVSLTLGTPTLPVWVNGSS 424

Qy 340 NNATFTPTVPVLLQILSGAQTAAQDLLPAGSVYPLPAHSTIEIT-----LPATALA 390

Db 425 INVMDKFKITVDYVI-----AQN-----TSYP-POANVITVNSVNMWYTLIENDPTG 470

Qy 391 P-GAPHPFLHGHAFAYV-----RSAG--STTYN------DPIPRDVTSTGTP 431

Db 471 PFSIPHPNHLHGHDFLVVGRSPDQAGVPTQRYRNRPNATDMALLKSSNPVRDVA- --LP 528

Qy 432 AAGDNVTIRFQTDNPGPWFLHCHIDFHLDAAGFAIYFAEDADVKA----- 475

Db 529 ANG-WLLIAFKSDNPGAMLFHCHIAWHVSGSLSVQYLERPNDRNGFSQADKNQHNNCN 587

```
QY 476 -----AANPVPKAWSDL 487
Db 588 AWRAYWPTNFPFKIDSL 605

RESULT 15
A36962
laccase (EC 1.10.3.2) precursor - fungus (Filobasidium floriforme) (ATCC 34873)
N;Alternate names: diphenol oxidase
C;Species: Filobasidium neoformans, Cryptococcus neoformans
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Mar-1998
C;Accession: A36962
R;Williamson, P.R.
J. Bacteriol. 176, 656-664, 1994
A;Title: Biochemical and molecular characterization of the diphenol oxidase of Cryptococcus
A;Reference number: A36962; MUID:94131944; PMID:8300520
A;Accession: A36962
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-624 <WIL>
A;Cross-references: GB:L22866
C;Genetics:
A;Gene: CNLAC1
A;Introns: 25/3; 69/3; 117/1; 137/3; 176/2; 204/2; 223/3; 238/3; 371/2; 391/2; 426/3; 55
C;Superfamily: laccase
C;Keywords: copper; glycoprotein; oxidoreductase

Query Match 22.8%; Score 608; DB 2; Length 624;
Best Local Similarity 30.3%; Pred. No. 6e-37;
Matches 161; Conservative 82; Mismatches 216; Indels 72; Gaps 19;

QY 10 VANAPSPDGLRDAIVNGVVPSPITGKGRFQNLNVVDTLTNHSMKASTSIHWGFF 69
Db 68 IAKAFSPDGYEREVYVNNMFPCPVTEANTGTIIHV-----NNHLDGQSLHWGLR 122
QY 70 QAGTNWADGPAFVNQCPIASGHSFLYDFHVPDQAGTFYHSHLSQYCDGLRGFFVYVDP 129
Db 123 QLGTAEMDGVPGITQCPPIPGGSEFTYFTVSHQSGTYWHSHYSNSMADGIWGPLIVHSP 182
QY 130 KDPHASRYDVNVESTVITLTDWHTAARL-----GPRFLGADATLINGLGRS 177
Db 183 NEPLQRGRDYD-EDRIVFITDMMHNDSEIIAALATPEGYKGNIAAPPQGDAILINGRQT 241
QY 178 ASTPTAALAV-----INVQHGKRYRFLRSLVSCDPNYTFSIDGHNLTVEVDGINSQP 230
Db 242 NCTATGSSSCFYPPPEIQVPVNCVRLRFISATAHPMYRISIDNHPMEVVEADGTAVYG 301
QY 231 LLVDSIQIFAAQRYSFVLNANQ-TVGN-YVVRANP----NFGTVGFAGGINSAILRYQGA 284
Db 302 PTVHEISVAPGERYSAINTEGKEGDAFWLRTSVALSCLMFGAVSQEG---LAVVRYTGN 358
QY 285 PVAEPTTTQTTS-----VIP---LIET-NLHPLARMPVPGSPTPGGVDKALNLF-- 330
Db 359 GNVSTEEPQISAWSDLAGVIVPCVGLDQTYTLSPRDSLSAPREPLQSHFFNSERGAFAVNV 418
QY 331 ---NFGNTNFTINNATPTPTVVLQLSQAQTAQDILLPAGSVYPLPAHSTIEITPAT 387
Db 419 LGNTFQGYGF--NNISYQNQIFNPLLSIVQRGSCENTLVSSRTFPDFGPGNIIINLDT 476
QY 388 ALAPGAPHPHLGHAFVAV-RSAGST-----YNYNDPIPRDVVSTGTGAAGDQVNT 438
Db 477 VI----DHPYHLRGNEFQVIGRGTCALSIDNLNTIDFTLDNPVRKDTLWI---QGGSWAV 529
QY 439 IRFQTDNPGPFLHCHIDFHLDAQ-FAIVFAEDVADYKAAANPVPKAWSDL 488
Db 530 LRITADNPGVWALHCHIGWHLTECKLAVIVVQPSAIGHMES--PESWTNLC 578
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Search completed: December 14, 2002, 08:29:03

Job time : 48 secs

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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:08:11 ; Search time 3052 Seconds
(without alignments)
14303.476 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgggccggtggcgag.....tgagcgaggctaaccagtga 1500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
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35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_higo_hum.*
40: em_higo_mus.*
41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1500	100.0	1500	6	AX384796	AX384796 Sequence
2	1500	100.0	1932	8	TU044430	U44430 Trametes ve
3	1399.2	93.3	2408	8	AY049725	AY049725 Trametes
4	913.2	60.9	1563	8	AF414109	AF414109 Trametes
5	911.4	60.8	1563	8	TVE18012	Y18012 Trametes ve
6	899.6	60.0	1618	6	E02618	E02618 DNA encodin
7	899.6	60.0	1618	6	E02625	E02625 DNA sequenc
8	897	59.8	1497	6	E02226	E02226 CDNA encodi
9	894.8	59.7	1618	6	E02617	E02617 DNA encodin
10	894.8	59.7	1618	6	E02624	E02624 DNA encodin
11	892.2	59.5	1497	6	E02225	E02225 CDNA encodi
12	874.8	58.3	1572	6	AX002145	AX002145 Sequence
13	871.6	58.1	1572	6	AX002146	AX002146 Sequence
14	866.6	57.8	1829	8	AF176230	AF176230 Polyporus
15	861.4	57.4	1739	3	AB006824	AB006824 Trachyder
16	852.6	56.8	1557	8	AB072703	AB072703 Pycnoporu
17	843	56.2	1557	8	AF152170	AF152170 Pycnoporu
18	837.6	55.8	1869	8	AF491759	AF491759 Basidiomy
19	825	55.0	2127	8	TU044851	U44851 Trametes ve
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21	771.8	51.5	2689	8	TMTLCCB	L49377 Trametes vl
22	771.8	51.5	2880	6	I65230	I65230 Sequence 3
23	755.4	50.4	7986	6	AX015224	AX015224 Sequence
24	729.8	48.7	2561	8	TU044431	U44431 Trametes ve
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29	525.4	35.0	1602	8	AB020026	AB020026 Pleurotus
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33	512.6	34.2	1713	8	POPOX2R	Z34848 P.ostreatus
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36	472.6	31.5	1170	6	AR096341	AR096341 Sequence
37	472.6	31.5	1170	6	ARI40077	ARI40077 Sequence
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ALIGNMENTS

RESULT 1
AX384796
LOCUS AX384796 1500 bp
DEFINITION Sequence 1 from Patent WO0196543.
ACCESSION AX384796
VERSION AX384796.1 GI:19577931
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1
AUTHORS Hood,E., Howard,J.A., Bailey,M., van Gastel,F.J., Ward,M., Wang,H. and Woodard,S.
TITLE Method of increasing recovery of heterologous active enzymes produced in plants

JOURNAL Patent: WO 0196543-A 1 20-DEC-2001;
 Prodigene, Inc. (US); Genencor, Inc. (US)
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CDS

BASE COUNT 275 a 551 c 402 g 272 t
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 Best Local Similarity 100.0%; Pred. No. 2.3e-216;
 Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Trametes versicolor laccase I (lccI) mRNA, complete cds.
 ACCESSION U44430
 VERSION U44430.1 GI:1172162
 KEYWORDS
 SOURCE Trametes versicolor.
 ORGANISM Trametes versicolor
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Aphyllophorales; Trametes.
 REFERENCE 1 (bases 1 to 1932)
 TITLE Ong, E., Pollock, W.B. and Smith, M.
 AUTHORS Cloning and sequence analysis of two laccase complementary DNAs
 from the ligninolytic basidiomycete Trametes versicolor
 JOURNAL Gene 196 (1-2), 113-119 (1997)
 MEDLINE 97464057

PUBMED 9322748
REFERENCE 2 (bases 1 to 1932)
AUTHORS Ong,E., Pollock,B. and Smith,M.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T 1Z3, Canada

FEATURES
Source Location/Qualifiers
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BASE COUNT 367 a 665 c 521 g 379 t

Query Match 100.08; Score 1500; DB 8; Length 1932;
Best Local Similarity 100.08; Pred. No. 2.2e-216; Indels 0; Gaps 0;
Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AY049725
LOCUS
DEFINITION
ACCESSION
VERSION

AY049725
Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.
2408 bp mRNA linear
PLN 13-SEP-2001
AY049725.1 GI:15617226

KEYWORDS

SOURCE Trametes versicolor.
ORGANISM Trametes versicolor.
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Trametes.
AUTHORS 1 (bases 1 to 2408)
TITLE McClean,K.H., O'Brien,M.M. and Dobson,A.D.W.
JOURNAL Trametes versicolor laccase (lacI) mRNA sequence
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 2408)
TITLE McClean,K.H., O'Brien,M.M. and Dobson,A.D.W.
JOURNAL Direct Submission
TITLE Submitted (31-JUL-2001) Microbiology, National Food Biotechnology Center, University College Cork, Cork, Ireland
JOURNAL Location/Qualifiers

FEATURES

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BASE COUNT 451 a 848 c 630 g 479 t
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Query Match 93.3%; Score 1399.2; DB 8; Length 2408;
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Db 1650 ATTGAGACGAACCTTCGACCCCTCGCTCGCATGCTGTGCTGCGACGCCGACACCGCGG 1709
Qy 961 GGGTGCACAAAGCGCTCAACCTCGGCTTAACTTCAACGGCACCAACTTCTTATCAAC 1020
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Qy 1021 AAGCGACTTTCAGCGCGCGACGCTCCCGGTACTCTCCAGATTCGAGCGGTGGCGAG 1080
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RESULT 4
AF414109          1563 bp      mRNA      linear      PLN 26-SEP-2001
LOCUS             Trametes versicolor laccase B precursor (lac1) mRNA, complete cds.
DEFINITION
ACCESSION         AF414109
VERSION           AF414109.1  GI:15778441
KEYWORDS
SOURCE
ORGANISM          Trametes versicolor.
                  Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                  Aphyllophorales; Trametes.
REFERENCE
  1 (bases 1 to 1563)
  Jollivalt,C., Madzak,C., Caminade,E. and Mouglin,C.
  2,5-xylidine induced laccase from the basidiomycete Trametes
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  Unpublished
JOURNAL
REFERENCE
  2 (bases 1 to 1563)
  Jollivalt,C., Madzak,C., Caminade,E. and Mouglin,C.
  Direct Submission
  Submitted (23-AUG-2001) Unite de Phytopharmacie, INRA, Route de
  Saint Cyr, Versailles 78026, France
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    YSLPSNADIEISFPATAAPGAPHPFLHGHAFVAVRSAGTVVYNDPIRFDVYSTG
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    sig_peptide     1..63
BASE COUNT       273 a 591 c 387 g 309 t      3 others
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Best Local Similarity 75.6%; Pred. No. 4e-128;
Matches 1131; Conservative 0; Mismatches 366; Indels 0; Gaps 0;
QY      4  ATCGGGCGGTGGCGAGCTCGTGTGCGGAACGCCGCCGCTTCGCCCGACGGCTTCCTT 63
DB      67  ATCGGTCCGCTGGCGCGCTAACTACCAACGACGCGGTGAGCCCGCGGTTTCT 126
QY      64  CGGGATGCCATCGTGTGTCACGGCTGGTCCCTTCCCCGCTCATCACCGGGGAAGGGA 123
DB      127  CGCAGCGCGTGTGTGAAACGGCGGCGACCCCTTGGCCCTTCTATCAGGGTAAACATGGGG 186
QY      124  GACCGTTCAGCTCAACCTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACT 183
DB      187  GATCGCTTCCAGCTCAATGTCGACACCACTTACCAACACACGATGCTGAAGACAGC 246
QY      184  AGTATCCACTGGACGGCTTCTTCAGGAGGAGGACCACTGGGAGAGACGCCCGGTTTC 243
DB      247  AGTATTCACTGGCAGCGTTTCTTCCAGAGGAGGACCACTGGGCGCGCGACGGTCCCGCTTC 306
244  GTCAACACAGTGGCCTATTGCTTCCGGGCATTCATTTCTGTACGACTTTCATGTGCCGAC 303
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424  GAGACACGCTCATCAGTTGACCGGCTGTACACACGCGCTGCCGGCTCGGTCCGACG 483
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544  ACCGCGCGCTTGTCTGTGATCAACGTCACGACGGAAGCGGTACCGCTTCCGCTCTCGTT 603
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607  ACCGCGGACCTCTCAGTTATCAGTGTACCCCGGGTAAACGCTACCGTTCCGCTGGTG 666
604  TCGATCTCGTGGACCGCAACTACAGTTTACAGATCGAGGGGACAACTGACCGCTATC 663
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667  TCCCTCTCGTGGACCGCAACTACAGTTTACAGATCGATGGTTCACAACATGACGATATC 726
664  GAGGTGCGAGGTATCAACAGCGGCTCTCTGTGCTGACTCTATCAGATCTTCGCGGG 723
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727  GAGACGACTCAATCAACAGCGGCGGCTCTGTGCTGCTTCAATTCAGATTTTCGCGCG 786
724  CAGCGCTACTCTCTTGTGTTGAATGCAACAAACGCTGGCAACTACTTGGTCCGCGG 783
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787  CAGCGTTACTCTCTGCTGTCGAGGCGCAACAGGCGCTCGACAACACTTGGATTCGCG 846
784  AACCCGAACTTGGAAAGGTTGGTTCGCGGGGGGATCACTCCGCCATCTCGCGCTAC 843
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1027  GTCGACCTGGCCATCAACATGGGTTCAACTTCAAGCGGACCACTTCTTCATCAACGC 1086
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1084  GCACAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
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1207  ATCTCTCTTCCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1266
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1267  CAGCGTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
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[illegible]

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RESULT 7
E02625
LOCUS E02625 1618 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence(OJ-POM2)coding for phenol oxidase.
ACCESSION E02625
VERSION E02625.1 GI:2170853
KEYWORDS JP 1990242685-A/2
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
REFERENCE
AUTHORS Kojima,Y. and Kita,Y.
TITLE RECOMBINANT DNA OF PHENOL OXIDASE, YEAST TRANSFORMED WITH SAME
RECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION OF PHENOL
OXIDASE
JOURNAL Patent: JP 1990242685-A 2 27-SEP-1990;
OJI PAPER CO LTD
COMMENT OS Coriolus hirsutus
PN JP 1990242685-A/2
PD 27-SEP-1990
PF 14-MAR-1989 JP 1989061859
PI KOJIMA YASUSHI, KITA YUKIO
PC C12N15/53,C12N1/19,C12N9/02,(C12N15/53,C12R1:645),(C12N1/19,
C12R1:865),
PC (C12N9/02,C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain-IFO 4917;
CC *source: library-plasmid pVC P02;
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FH CDS 56..1618
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FT FT /gene='OJ-POM2'.
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BASE COUNT 285 a 589 c 403 g 341 t
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Best Local Similarity 75.0%; Pred. No. 4.4e-126;
Matches 1124; Conservative 0; Mismatches 374; Indels 0; Gaps 0;

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RESULT 8
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 LOCUS cDNA encoding phenol oxidase. 1497 bp RNA linear PAT 29-SEP-1997
 DEFINITION
 E02226
 VERSION 1 GI:2170464
 JOURNAL JP 1990027986-A/2
 KEYWORDS
 SOURCE Coriolus hirsutus.
 ORGANISM Coriolus hirsutus.
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Aphyllophorales; Coriolus.
 Kojima,Y., Shinohara,Y., Hirayanagi,M., Tsukamoto,A., Suglura,J.,
 Sakano,M., Kita,Y. and Koida,K.
 PHENOL OXIDASE GENE (II)
 PATENT: JP 1990027986-A 2 30-JAN-1990;
 OJI PAPER CO LTD
 OS Coriolus hirsutus
 PN JP 1990027986-A/2
 PD 30-JAN-1990
 PF 15-JUL-1988 JP 1988175236
 PI KAJIMA YASUSHI, SHINOHARA YUKIKO, HIRAYANAGI MIEKO, PI
 TSUKAMOTO AKIRA,
 SUGIURA JUN, SAKAINO MAKOTO, KITA YUKIO, KOIDE KAZUO PC
 C12N15/53/C12N9/02.(C12N15/53,C12R1:645);
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Best Local Similarity 74.9%; Pred. No. 1.le-125;
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RESULT 9
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LOCUS E02617 1618 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding phenol oxidase(II).
ACCESSION E02617
VERSION E02617.1 GI:2170845
KEYWORDS JP 199023885-A/1.
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
Sugiura, J., Tsukamoto, A. and Kita, Y.
PHENOL OXIDASE GENE RECOMBINATION DNA, MICROORGANISM TRANSFORMED
WITH SAME RECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION
OF PHENOL OXIDASE
Patent: JP 199023885-A 1 21-SEP-1990;
OJI PAPER CO LTD
OS Coriolus hirsutus
PN JP 199023885-A/1
PD 21-SEP-1990
PF 13-MAR-1989 JP 1989057952
PI SUGIURA JUN, TSUKAMOTO AKIRA, KITA YUKIO
PC C12N1/53, C12N1/21, C12N9/02, (C12N1/21, C12R1/19), (C12N9/02, PC
C12R1/19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FT CDS 56..1618
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Best Local Similarity 74.8%; Pred. No. 2.3e-125;
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KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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E02624
DNA sequence(OJ-POM5) coding for phenol oxidase.
PAT 29-SEP-1997
E02624
GI:2170852
JP 1990242685-A/1.
Coriolus hirsutus.
Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
Kojima,Y. and Kita,Y.
RECOMBINANT DNA OF PHENOL OXIDASE, YEAST TRANSFORMED WITH SAME
FECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION OF PHENOL
OXIDASE
Patent: JP 1990242685-A 1 27-SEP-1990;
QJI PAPER CO LTD
Qs Coriolus hirsutus
PN JP 1990242685-A/1
PD 27-SEP-1990
PF 14-MAR-1989 JP 1989061859
PI KOJIMA YASUSHI, KITA YUKIO
FC C12N15/53,C12N1/19,C12N9/02,(C12N15/53,C12R1:645),(C12N1/19,
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CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain-IFO 4917;
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Best Local Similarity 74.8%; Pred. No. 2.3e-125;
Matches 1121; Conservative 0; Mismatches 377; Indels 0; Gaps 0;
Qy 1 GCATCGGCGCGTGGCGAGCGCTCGTCGCGAAGCCCGCTCGCTCGCGCAGCGCTTC 60
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DEFINITION E02225
ACCESSION E02225
VERSION E02225.1 GI:2170463
KEYWORDS JP 1990027986-A/1.
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
REFERENCE 1 (bases 1 to 1497)
AUTHORS Kojima, Y., Shinohara, Y., Hirayanagi, M., Tsukamoto, A., Sugiyama, J., Sakaino, M., Kita, Y. and Koide, K.
TITLE PHENOL OXIDASE GENE (II)
JOURNAL Patent: JP 1990027986-A 1 30-JAN-1990;
OJI PAPER CO LTD
COMMENT OS Coriolus hirsutus
PN JP 1990027986-A/1
PD 30-JAN-1990
PF 15-JUL-1988 JP 1988175236
PI KAJIMA YASUSHI, SHINOHARA YUKIO, HIRAYANAGI MIEKO, PI TSUKAMOTO AKIRA,
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C12N15/53/C12N9/02, C12N15/53, C12R1:645;
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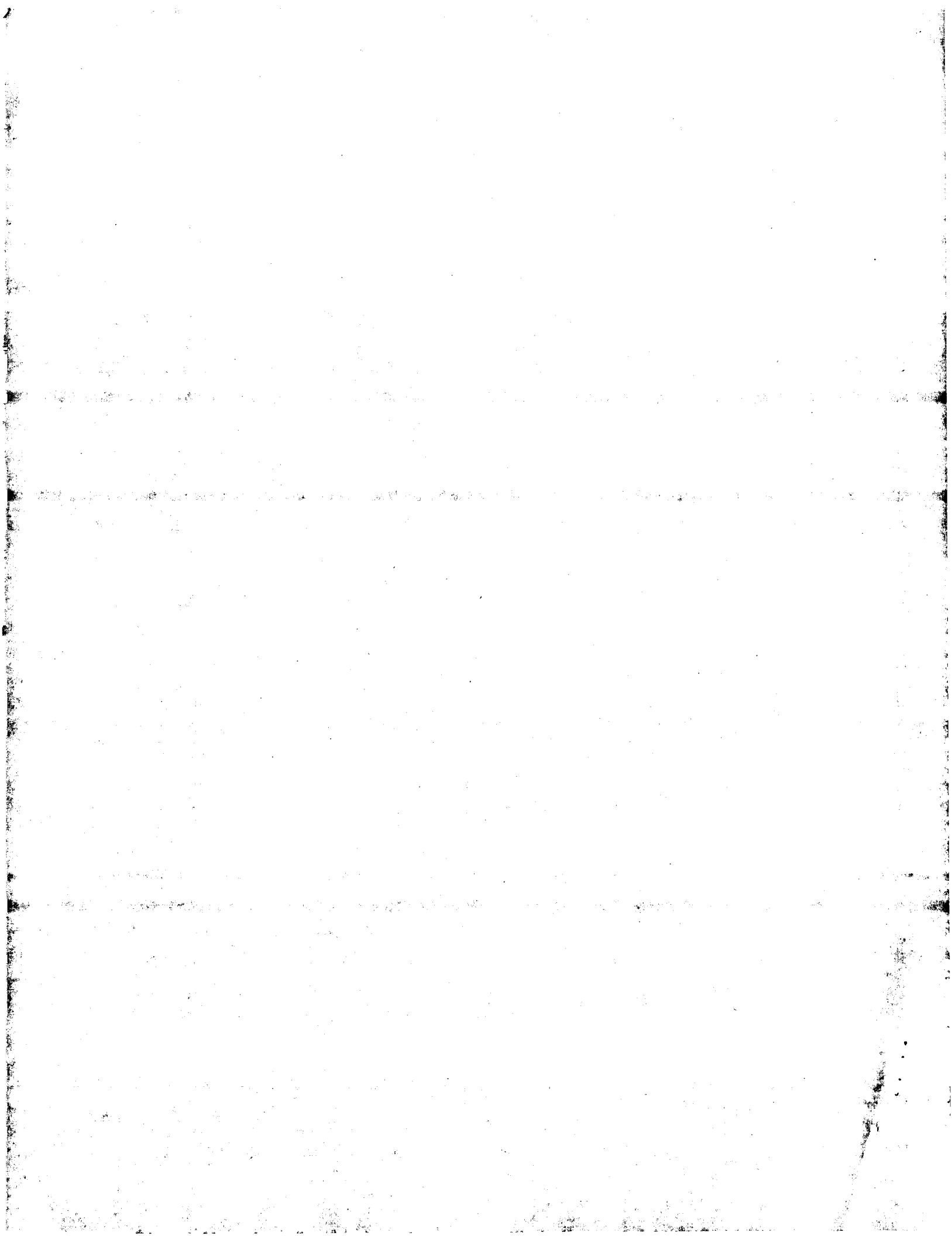
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Matches 1119; Conservative 0; Mismatches 378; Indels 0; Gaps 0;
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ACCESSION AB006824
VERSION GI:3176127
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REFERENCE 1 (sites)
AUTHORS Iwamoto,H., Watanabe,H., Minakami,M., Hirose,J., Hiromi,K.,
Mukai,H., Yoshioka,H. and Kato,I.
TITLE Purification, Characterization, and Molecular Cloning of Bilirubin
Oxidase from Trachyderma tsunodae K-2593
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1739)
AUTHORS Iwamoto,H.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1997) Hiroyuki Iwamoto, Fukuyama University,
Faculty of Engineering, Gakuen-cho, Fukuyama, Hiroshima 729-02,
Japan (E-mail:iwamoto@fubac.fukuyama-u.ac.jp, Tel:0849-36-2111,
Fax:0849-36-2023)
FEATURES
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NDSTVITLADWYHVAARLGRPRPLGADSTVINGLSLSTPNADLAVISVTOGKRYR
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VIELPASTIELTLPATVPAPVPHFLHGHTFAVRSAGSTAYNDPNLRWDVST
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polyA_signal 1717..1722
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BASE COUNT 351 a 587 c 416 g 385 t
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Best Local Similarity 73.8%; Pred. No. 2.4e-120;
Matches 1109; Conservative 0; Mismatches 391; Indels 3; Gaps 1;
Qy 1 GCATCGGGCGGCTGGGACGCTCTGCTCGCGAAGCCGCCCTCTCGCCGAGGCTTC 60
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Db 76 GGGCTTGGCCCTCTGTGTCGACCTCACTGTCTCCAAGCCGCTTATCTCCCGATGGCTTT 135
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Qy 61 CTTCGGGATGCCATCGTGGTCAACGGGCTGCTCCCTTCCCGCTCATCAACCGGGAAGA 120
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Qy 121 GGAGACCGCTTCAGACTCAACGCTGCTGACACCTTGACCAACACACAGCATGCTCAAGTCC 180
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Db 196 GGGACCGCTTCCAGCTTAATGTGATCGACAACATGACGAACACACACATGCTGAATCG 255
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Qy 181 ACTAGTATCACTGGCACGCTTCTTCCAGGAGGACCAACTGGGCGAGACGGACCGCG 240
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Db 256 ACGAGCATTCATGGCACGCTTCTTCCAGAGGAACTAACTGGGCGGAGGTGTGCT 315
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Qy 241 TTGCTCAACAGTCCCTTATTGCTTCCGGCATTTCTGTACGACTTCCATGTGCC 300
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Db 316 TTTGTTAATCAATGCCCATCGCCCCGGGCATTTGTTCTCTACGACTTCCGGGTCCCT 375
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Qy 301 GACGAGCAGAGAGTCTGTGTACCAAGATCATCTGTCTAGGCAATACTGTGACGGGCTG 360
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Qy 361 CGAGACCGTTCGCTGTGTAGCACCCCAAGATCCGACGCGCCGCTACGATGTTGAC 420
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Db 436 AGAGCTCTATGTGCTTACGACCCCAATGATCCACATGAGATTTGTATGATGTGAC 495
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Qy 421 AACGAGACGCTCATCACGCTTGACGACTGTGTACCAACCGCTCCCGGCTCGGTCCC 480
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Db 496 AACGATTCACCGCTCATAAACCTTGGCAGACTGTGTACCAAGTTGCGAGCGAGCTTTGGCCCA 555
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Qy 481 AGTTCCGACTCGGCGGAGCCACGCTCATCAATGGTCTTGGGCGGTGGGCTCCACT 540
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Db 556 GGTTCGCCACTCGGGGAGACTCAACAGTAAATCAACGCTCTTGGCGCTTCCCTCAGTACT 615
|||||
Qy 541 CCCACCGCGGCTTGTGTGTATCAACGCTCCAGCACGGAAGAGCGCTACCGTTCGGTCTC 600
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Db 616 CTAACGAGATCTGGCGGTGATATCGGTACACCAAGGAACGTTACCGCTTCCGGCTTG 675
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Qy 601 GTTTCGATCTCGTCGACCCCGAATACAGTTCAGCATFCGAGGGGACAACTCTGACCGTC 660
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Db 676 ATATCCCTGTCTATCGACCCGTTCCACACCTTCAGCATCGAGGTCATGACTTACTATC 735
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Qy 661 ATCAGGCTCGACGCTATCAACAGCAGCCTCTCTGTCGACTTATCAGCATCTTCGCC 720
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Qy 721 CGCAGCGCTACTCTTGTGTGTAATCGAACAACAGCGTCGGCACTACTTGGTTCGCG 780
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Db 796 GCACGCTACTCTCTGTTCTTAGCGCGGTCAAGGACATCGAACAATACTGGATCCG 855
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Qy 841 TACCAAGCGGACAGTCCGCGAGCCCACTAGACCCACAGACAC---GTCGGTGATCCCG 897
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Db 976 TTGCTCGAGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:09:06 : Search time 2135 Seconds
(without alignments)
11378.562 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgggccggtggcgag.....tgagcaggcctaaccagtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.8	10.0	486	9	AT005119
2	138.8	9.3	419	9	AT004146
3	97	6.3	953	17	CNS0624A
4	90	6.0	501	9	AU082584
5	90	6.0	1020	17	CNS062GE
6	78.4	5.2	894	10	BE216612
					HV_CEB001

7	72	4.8	612	14	B0826969
8	69.4	4.6	740	14	B0839421
9	69	4.6	509	13	BJ270853
10	69	4.6	511	13	BJ279320
11	68.4	4.6	509	14	B0760633
12	68.4	4.6	663	14	B0750959
13	68.2	4.5	519	10	AW671756
14	67.8	4.5	1003	17	CNS06601
15	67.6	4.5	662	13	BJ959707
16	67	4.5	679	12	BE905538
17	66.6	4.4	790	10	BE040626
18	66.4	4.4	565	14	B0764122
19	66	4.4	429	12	BF201692
20	66	4.4	575	13	BJ255523
21	66	4.4	641	13	BJ959316
22	65.4	4.4	627	13	BJ246521
23	64.6	4.3	539	14	B0578129
24	64.6	4.3	578	17	BH785519
25	64.6	4.3	627	17	AQ399182
26	64.4	4.3	440	10	B8423544
27	64.2	4.3	607	13	BM318801
28	63.2	4.2	617	13	BJ289468
29	63.2	4.2	734	13	BJ295794
30	62.8	4.2	453	12	BG060868
31	62.8	4.2	640	10	BE360607
32	62.6	4.2	843	17	CNS00CS1
33	62.2	4.1	461	14	B0578036
34	62.2	4.1	844	10	B8430514
35	62	4.1	655	13	BM370593
36	61.8	4.1	987	14	BQ752322
37	61.6	4.1	383	13	BJ281253
38	61.6	4.1	631	13	BJ277128
39	61.6	4.1	639	10	BE360567
40	61.2	4.1	332	13	BJ286316
41	60.6	4.0	526	12	BG906020
42	60.6	4.0	559	13	BM418197
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45	60	4.0	476	6	BM441946

ALIGNMENTS

RESULT 1
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LOCUS AT005119 POMF01 Pleurotus ostreatus cDNA clone MFB11-A12, mRNA 486 bp linear EST 25-MAR-2002
DEFINITION AT005119 sequence.
ACCESSION AT005119
VERSION AT005119.1 GI:13419977
KEYWORDS EST.
SOURCE oyster mushroom.
ORGANISM Pleurotus ostreatus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Pleurotaceae; Pleurotus.
REFERENCE 1 (bases 1 to 486)
AUTHORS Lee,S.H., Kim,B.G., Kim,K.J., Lee,J.S., Yun,D.W., Hahn,J.H., Kim,G.H., Lee,K.H., Suh,D.S., Kwon,S.T., Lee,C.S. and Yoo,Y.B.
TITLE Comparative Analysis of Sequences Expressed during the Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus ostreatus
JOURNAL Fungal Genet. Biol. 35 (2), 115-134 (2002)
MEDLINE 21838565
COMMENT Contact: Beom-Gi Kim
Division of applied microbiology
Institute of Agricultural Science and Technology(NIAST)
249 Seodundong Kweonseonku, Suwon 441707, Korea
Tel: 32-331-290-0347
Fax: 32-331-290-0399
Email: bgkimyes@da.go.kr
Submitted through BRIC(Biological Research Information Center) of Korea

URL: http://bric.postech.ac.kr/
GeneNuri No. KS105130.
Location/Qualifiers
1. 486

FEATURES
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/dev_stage="mature fruiting body"
/lab_host="E.coli"

/note="Vector: lambda triPEX2; Site_1: SfiIA; Site_2: SfiIBI; average insert size:1500 bp; initial pfu: 5 * 10⁷; Isolation of total RNA from the mature fruiting body cultivated in poplar tree sawdust bottle"

BASE COUNT
ORIGIN

94 a 141 c 111 g 140 t

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Best Local Similarity 68.2%; Pred. No. 5.2e-22;
Matches 208; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Db 182 ACCGGTCAATTTCCCTGGTCCCTCATCATCTGGGAACAAGGTGACCAATTTTCAGATTAAT 241

QY 142 GTCGTGCACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGCAGCGC 201

Db 242 GTAATTGACGAGTTGGTCGACACATCGATGCTTCTGGACACAAGTATCCACTGGCATGGC 301

QY 202 TTCCTCAGGAGGACCAACTGGGACAGACCGCGGTTGTCACACAGTGCCTATT 261

Db 302 TTCATATCAAGGAAGCAACTGGGCTGACGGGCTGCTTCGTACTCAATGTCTATC 361

QY 262 GCTTCGGGCGATTCATTTCTGTAGACTTCCATGTCGCCGACGAGGAGACGTTCTGG 321

Db 362 GTCCGGGAGACTCTTCTGTACTCATTTTCGGCTCCTGATCAGCGGACATCTCG 421

QY 322 TACCACAGTCACTGTCTACCAATCTGTGACGGGTGCGGAGGACCGCTTCTGCTGTAC 381

Db 422 TATCACTCGCATCTCTCGACGAGTATTGCGACGAGTACGTGGTGTCTTGTGCTGTAC 481

QY 382 GACCC 386
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Db 482 GACCC 486

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LOCUS AT004146 419 bp mRNA linear EST 25-MAR-2002
DEFINITION AT004146 POSLM01 Pleurotus ostreatus cDNA clone 1448LM, mRNA sequence.

ACCESSION AT004146

VERSION AT004146.1 GI:13419004

KEYWORDS EST.

SOURCE Oyster mushroom.

ORGANISM Pleurotus ostreatus

REFERENCE 1 (bases 1 to 419)

AUTHORS Lee, S.H., Kim, B.G., Kim, K.J., Lee, J.S., Yun, D.W., Hahn, J.H., Kim

, G.H., Lee, K.H., Suh, D.S., Kwon, S.T., Lee, C.S. and Yoo, I.B.

Comparative Analysis of Sequences Expressed during the

Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus

ostreatus

Fungal Genet. Biol. 35 (2), 115-134 (2002)

CONTACT: Beom-Gi Kim

Division of Applied Microbiology

Institute of Agricultural Science and Technology (NIAT)

249 Seodundong Kweonseonku, Suwon 441707, Korea

Tel: 82-331-290-0347

Fax: 82-331-290-0399

Email: bgkimyes@da.go.kr
GeneNuri No. KS104602
Submitted through BRIC (Biological Research Information Center) of Korea

URL: http://bric.postech.ac.kr/.

FEATURES
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/lab_host="E.coli"
/note="Vector: lambda Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI; average insert size:1000 bp; initial pfu: 5 X 10⁷; Library information: Isolation of total RNA from the mycelia incubated in shaking liquid MCM media at 30 deg C"

BASE COUNT 84 a 129 c 103 g 103 t

ORIGIN

Query Match 9.3%; Score 138.8; DB 9; Length 419;

Best Local Similarity 62.6%; Pred. No. 1.1e-19;

Matches 253; Conservative 0; Mismatches 142; Indels 9; Gaps 2;

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QY 1069 AGCGGTGGCGAGACGACAAAGACCTGCTCCCTGAGCTCTGTCTACCGCTCCGCC 1128

Db 66 TCGGACACACGCGATGCGCATGATCTGCGCCCTGCTGGATCAATTTATGACATCAAGCTG 125

QY 1129 CACTCCACATCAGATCACGCTGCGCGACGCGCTTGGCCCGGGTGACCGCACCC 1188

Db 126 GGAGACGTCGTGAGATCACATGCTGCTCCCTCGTATTTCG-----TGGACCGCACCC 179

QY 1189 TTCACCTGACGCTGACGCTTTCGCGGTTCGTCAGCGGGGAGACACCACTATTAAC 1248

Db 180 CTCATTTACATGGGACATCTTCGCGTAGTTCGTCAGTCGCGCAGCAGCGCTTACAC 239

QY 1249 TACAACGACCGATCTTCGCGGAGCTGTCGAGAGGCGACGCGCGCGGGGAGACAC 1308

Db 240 TACGAGAACCCCGTCGTCAGGATGTCGTATCCATCGTCGATGACCCCAACG---GACAA 296

QY 1309 GTCAGATCCGCTTCCAGACGACAAACCCGCGCGTTCCTCCACTGCCACATCGAC 1368

Db 297 GTCACATCCGATTCGTAGACAGACACGAGTCATGTTCCCTCCATTCACATCGAC 356

QY 1369 TTCACCTGACGCGGGCTTCGCGATCGTGTTCGAGAGGACGT 1412

Db 357 TGGCATCTTGACCTGGCTTCGCTGCTGCTTCGCCGAAGGAGT 400

RESULT 3
CNS06244/c 953 bp DNA linear GSS 06-JUL-2001
LOCUS T7 end of clone AY0AA015E06 of library AY0AA from strain CBS 6340
DEFINITION of Kluyveromyces thermotolerans, genomic survey sequence.

ACCESSION AL421856

VERSION AL421856.1 GI:12205051

KEYWORDS GSS.

SOURCE Kluyveromyces thermotolerans.

ORGANISM Kluyveromyces thermotolerans

REFERENCE 1 (bases 1 to 953)

AUTHORS Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,

Bolotin-Fukuhara, M., Bon, E., Brattier, P., Casaregola, S.,

de-Montigny, J., Dujon, B., Durans, P., Lepingle, A., Lorente, B.,

Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,

Saurin, W., Tekalia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,

Wincker, P. and Weissbach, J.

TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE	20584711
PUBMED	11152876
REFERENCE	2 (bases 1 to 953)
AUTHORS	Malpartuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P. and Dujon,B.
TITLE	Genomic exploration of the hemiascomycetous yeasts: 10.
JOURNAL	Kluyveromyces thermotolerans
MEDLINE	20584720
PUBMED	11152885
REFERENCE	3 (bases 1 to 953)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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	/clone_lib="AY02A"
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misc_feature	complement(<7. .879)
	/note="similar to Saccharomyces cerevisiae ORF YMR058w [FET3 ; cell surface ferroxidase, high affinity]"
	/evidence=not experimental
BASE COUNT	197 a 258 c 258 g 239 t
ORIGIN	1 others
Query Match.	6.5% ; Score 97; DB 17; Length 953;
Best Local Similarity	50.2% ; Pred. No. 1.2e-10;
Matches	343; Conservative 0; Mismatches 310; Indels 30; Gaps 3;
Qy	73 ATCGTGTCAACGCGGTGGTCCCTTCCCGCTCATCACCGGGAGAGGGACCGGCTTC 132
Db	
Qy	771 ATCAGTGTATGAGAGTTCATGTCGCCGACGTGCGGTCAAGAGGGCGACCGATC 712
Qy	133 CAGTCTAACGTCGTCGACACCTTGACCAACGACAGCATGCTCAAGTCCATAGTAGTCCAC 192
Db	
Qy	193 TGGCACCGGCTCTTCAGGAGGACGACCACTGGCGACAGGACCCGGGTTCGTCAACACG 252
Db	
Qy	663 TTCCATCGGGTGTTCAGAGACGGGACCACTCCATGACGCGCCCTCCCAATGGTGGTCAG 604
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Qy	253 TGCCCTATTGCTCCGGGCATTCATTTCTGTACGACTTCATGTGCCCGACCGACGAGCA 312
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Qy	603 TGCCCCATCGGGCTGGCGACACCTTCTGTACAACTTCACGGTGGATGACACGTGGCG 544
Qy	313 ACGTTCGTGGTACCACTCATCTGTCTACGCAATFACGTGACGGGCTGCGAGGACCGCTTC 372
Db	
Qy	543 ACGTACTGGTACCACCTCCGACACTTCGCGGGCAGTATCAGGACCGTATGCGGGTGCCTTT 484
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Qy	373 GTCGTGTACGACCCCAAGGATCCGACGCCAGCGGTACGATGTTGACACAGGACGACG 432
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Qy	483 GTGATTGAAGACGATGACTTTCATACGAC-----TACGATGAGGACGCT 439
Qy	433 GTCATCAGTTGACCGACTGGTACCA---CACGCGTCCCGGCTCGGTCCGAGGTTCCCA 489

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QY 643 GGCACAATCTGACCGTCATCGAGTCGACGGGTATCAACAGCAGCGCTCTCTTGTGCAC 702
Db 181 GGGCACAAGATGACGGTGGTGGAGCGGACGGGACCGACGCTGGCGGTCGTGGTGCAC 240
QY 703 TCTATCAGATCTTGGCGCGACGCGTACTCTCTTGTGTGTAATCGGAACCAACAGGTC 762
Db 241 GACATCGACATCTACTCGGCGAGAGTACTCTCGCTCTCTCTNAAGGCGGACGAGAGCGG 300
QY 763 GGCACAATCTGAGTGGTCCGCG 781
Db 301 GCGAGCTACTGGATCTCCG 319

RESULT 5
CNS06ZGE 1020 bp DNA linear GSS 06-JUL-2001
LOCUS T7 end of clone XAY0AA002D03 of library XAY0AA from strain CBS 6340
DEFINITION of Kluyveromyces thermotolerans, genomic survey sequence.
ACCESSION AL422292
VERSION AL422292.1 GI:12205486
KEYWORDS GSS.
SOURCE Kluyveromyces thermotolerans.
ORGANISM Kluyveromyces thermotolerans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
REFERENCE 1 (bases 1 to 1020)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Maupertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
GENOMIC exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
11152876
2 (bases 1 to 1020)
Maupertuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P.
and Dujon,B.
GENOMIC exploration of the hemiascomycetous yeasts: 10.
Kluyveromyces thermotolerans
FEBS Lett. 487 (1), 61-65 (2000)
20584720
11152885
3 (bases 1 to 1020)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. Hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
Location/Qualifiers
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/strain="CBS 6340"
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FET5 : multicopy oxidase ]"
/evidence=not_experimental

misc_feature
source

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BASE COUNT 267 a 249 c 236 g 261 t 7 others
ORIGIN
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Best Local Similarity 52.6%; Pred. No. 3.7e-09;
Matches 192; Conservative 1; Mismatches 172; Indels 0; Gaps 0;
QY 73 ATCGTGTGTCAAACGGCGTGGTCCCTTCCCGCTCATCATCCCGGGAAGAGGAGGACCGGCTTC 132
Db 474 ATTGGGTTCAACGGAGTKNGCGCGCCCTTGACATCCACCTAACRAAGGCGGATCGCTT 533
QY 133 CAGCTCAACGTCTGTGACACCTTTCACCAACCAACAGATGCTCAAGTCCACTAGTATCCAC 192
Db 534 ATTTTACGCTGACTAATGCTTCGAGAACCTGACAACTTCTTGTGCACTTCCATGTTGTTG 593
QY 193 TGCACGGCTTCTCCAGGAGGACCACTGGGCGAGACGCGCGGTTCGTCACACAG 252
Db 594 TCGCAATATATCAGGAGGCAACTTGAACCAAGATGAGCGGACTGAATATGGTGACACAG 653
QY 253 TGCCTATTGCTTCCGGGCAATTCATTTCTGTACGACTTCCATGTGCCCGACGAGGACGA 312
Db 654 TGTCCGATCATGCCAGGCGACACTTTGTTTACAACCTTACCGGTACCATGATCAGGCAGGT 713
QY 313 AGCTTGTGTACACAGTATCTGTCTACGAATATCTGTACGGCTGCGAGGACCGTTC 372
Db 714 ACTTCTGTGTACCACTCGCACTCTGCGCGCGAGTACACAGCGGTATGCGAGCGCGCTA 773
QY 373 GTCGTGTACCAACCCCAAGGATCGCAGCGCGCTACGATGTTGACAAACGAGAGCAGC 432
Db 774 ATTATCCAGATGACGATGATGACCGCTTGTGATGACGAGGAGATGGTCACTCCAGGTAACA 833
QY 433 GTCAT 437
Db 834 GACCT 838

RESULT 6
BE216612 894 bp mRNA linear EST 23-OCT-2001
LOCUS HV_CEB0010P08f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEB0010P08f, mRNA sequence.
ACCESSION BE216612
VERSION BE216612.2 GI:13265000
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 894)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frishch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
Unpublished (2001)
On Jul 3, 2000 this sequence version replaced gi:8904224.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 419
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 543.
Location/Qualifiers
1..894
/organism="Hordeum vulgare"
/cultivar="C116151 (Mla6)"
FEATURES
source

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/db_xref="taxon:4513"
/clone_lib="HVC0010P08"
library HVC0010P08
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give phagescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)
180 a 291 c 256 g 164 t 3 others

Query Match 5.2%; Score 78.4; DB 10; Length 894;
Best Local Similarity 54.8%; Pred. No. 1.1e-06;
Matches 204; Conservative 0; Mismatches 153; Indels 15; Gaps 2;
QY 25 GTCGTGCGGACGCCCCCTCTCGCCGACGCTTCCTCGGGATGCCATCGTGGTCAAC 84
DB 214 GACATCTGTACCAAGTACCAAGTCCCGGACTGCTTCGAGAAGCTCCCGTACCGTCAAC 273
QY 85 GCGGTGTCCTTCCCGCTCATACCGGGGAAGAGGACCGCTTCCAGCTCAACGTC 144
DB 274 GCGAGGCGCGCGCCGACCATCCGCGCCACGAGGCGA-----CACCATC 321
QY 145 GTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGGACGCTTC 204
DB 322 GTCGTCAACGTCCACAAAGGCTCGAGACCGGAGAACCGCCATCCACTGGCAGCGCATC 381
QY 205 TTCCAGGAGGACCAACTGGGCGAGACCGCGCTTCTCAACAGTCCCTATTGCT 264
DB 382 CGCCAGATTGACACCGCGTGGCTGACGCGCTGCGCGGCTGACGAGTCCCGATCCCT 441
QY 265 TCCGGCATTCATTCTTGACGACTTCCATGTGCCGACAGGACGAGGACGTTCTGGTAC 324
DB 442 CCGCGGAAACCTTCGCTTACAAATTC---GTGCTGCGACAGGCGCTGGCAGCTACGTTAC 498
QY 325 CACAGTCACTCTACGCAATACTGTGACGGGCTGCGAGGACCGTTCGTCGTGTACGAC 384
DB 499 CATGCGCACTAGGNNATGACGCGCTGGCGGNGCTCAACGGCATGATGCTGTGTCAGAGTG 558
QY 385 CCAAGGATCCG 396
DB 559 CCGCGGCGATCG 570

RESULT 7
BQ826969
LOCUS 612 bp mRNA linear EST 07-AUG-2002

DEFINITION
q49g07.x1 Moss EST library PPAS Physcomitrella patens cDNA clone
L-ASCORATE OXIDASE PRECURSOR 3', similar to SW:ASO_TOBAC Q40588
BQ826969
VERSION BQ826969.1 GI:22132079
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens.
REFERENCE
AUTHORS Quatrano, R., Bashardes, S., Cove, D., Cumig, A., Knight, C., Clifton
, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
Stepoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
, Waterston, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
COMMENT
JOURNAL
Leeds/Wash U Moss EST Project
Contact: Ralph Quatrano
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 430.
Location/Qualifiers
1. 612

Source
/organism="Physcomitrella patens"
/db_xref="taxon:3218"
/clone="PEP_SOURCE_ID:PPAS021314"
/clone_lib="Moss EST library PPAS"
/dev_stage="protonemal", 7day old ABA-treated"
/lab_host="E.coli DH10b"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
EcoRI; 7-day-old protonemal tissue was incubated 10-4M ABA
for 16 hours before RNA isolation. cDNA was synthesized
from Amersham's cDNA Synthesis Plus kit and ligated with
EcoRI-NotI linkers for cloning in the EcoRI site of Lambda
ZapII (Stratagene). After packaging, the library was
propagated in E. coli XL-I Blue cells and amplified. The
library was excised by mass excision in SOLR cells and
ampicillin resistant transformants selected. Approximately
, 1,000,000 colonies were grown and recovered. The double
stranded plasmid library was recovered and used to
transform DH10b cells by electroporation. Clones
corresponding to abundant transcripts were identified by
colony hybridization using a cDNA probe derived from
untreated protonemal tissue, and eliminated from the
library, by rearraying."
BASE COUNT 128 a 198 c 152 g 134 t

Query Match 4.8%; Score 72; DB 14; Length 612;
Best Local Similarity 53.1%; Pred. No. 2.3e-05;
Matches 153; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
QY 485 TCCCACTCGCGGAGCGCCGCTCATATGTTCTTGGCGGTGGGCTCCACTCCCA 544
DB 236 TTCCACAGAATGCCACCTGCGCCCTGGCTGCTGCTGCAATCCGACGCCCA 295
QY 545 CGCGCCGCTTGTGTGATCAACGCTCCAGCAGGAAGCGCTACCGCTCCGCTCGTT 604
DB 296 GATCGCACCTCATGTGTTGCCAGTCACCTCTGGAAAGAGCTACCGCTTCGCCGATCGCCA 355

```

QY 605 CGATCTCGTGGACCCGAACTACAGTTTACGATCGAGCGGCAACAATCTGACCGTCACTG 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 CGGTGGGTCCCTGCTCACTTATCTTGTGAGGCCATATAATGACGTGTCTC 415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 665 AGGTGCGAGGTATCAACAGCAGCCTCTCTTGTGCTACTTATCCAGATCTTCGCCGGC 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 AAGCCGACGCTCGCAAGCTCCAGCTTTCGTGCTCGCAATCTCTGGATGTGTATTCTGGTC 475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 725 AGCGCTACTCTCTTGTGTAATCGGAACCAACGGTCCGCAACTACT 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 AGAGTTAGGACGCTGTCTACCGCCCAACAGAGCGCTCAAGAACT 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
B0839421 740 bp mRNA linear EST 08-AUG-2002
LOCUS WHE4165_H08_P15S wheat CS whole plant cDNA library Triticum
DEFINITION aestivum cDNA clone WHE4165_H08_P15, mRNA sequence.
ACCESSION B0839421
VERSION B0839421.1 GI:22143743
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 740)
Lazo, G.R., Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Chinese Spring whole plant cDNA library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1..740
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4165_H08_P15"
/clone_lib="Wheat CS whole plant cDNA library"
/tissue_type="Roots, leaves, crown, stem and sheath"
/dev_stage="Adult"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, stem and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give pBluescript SK(-) phagemids in J. Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT 127 a 311 c 182 g 120 t
ORIGIN
Query Match 4.6%; Score 69.4; DB 14; Length 740;
Best Local Similarity 46.0%; Pred. No. 8.6e-05;
Matches 278; Conservative 0; Mismatches 321; Indels 6; Gaps 1;

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```

QY 423 CGAGAGCACGCTCATCAGTTGACCGCTGTACCAACACGCTGCCGGCTCGGTCCAG 482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 CGAGTGTGGACATGAACCCCATCGAGCTATCCCGCACCGCAGCGGTGTCAGC 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 483 GTTCCCACTCGGGCGGACCGCAGCTCATCAATGTTGTTGGGGGTGCGGCTCCATCC 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 TCCCAAGCTCTCGGACGCCATCCGTCACGGTCAACGGCAACCGGGACCTTACAACTGCTC 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 543 CACGCGCGCTTGTGTGATCAACGTCACAGCAGCGGAAAGCGTACCGCTTCGCTCGT 602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 CTCCCAAGACAGCGCGTGTTCGGGTCAAGTCGGGGAGACCAACCTATTCGCTTCAT 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 603 TTCGATCTCGTGGACCCGAACCTACAGTTTACAGATCGAGGGCACAAATCTGACGCTCAT 662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 CAACGCGCGCTCAACACCGAGCTCTTCGTCCTCCCTCGCGGCCACACCATGACCGTCT 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 663 CGAGGTGAGGTATCAACAGCAGCCTCTCTTGTGCTACTCTATCCAGATCTTCGCGGC 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 GGGCGCGCAGCGCTCTACCTCAAGCGCTACAAGCCACTGTCTATCGTCTGGGCGCTGG 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 723 GCAGCGTACTCTCTTGTGTTGAATCGAACCAACGTCGCAACTACTGGGTCCGCGC 782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 CCAGACACGAGCTCTCTGCTACTTTTCGACACCGCGCGGCTACTACTTCGCGC 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 783 GAACCCGAACCTTCGGAACGGTTGGTTCGCGGGGGGATCAACTCCGCTATCTTCGCGCTA 842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 TCGCGCTTAGCCAGCGCGAGGCGTGCCTTCGACAACACCAACCAACCGCATCTT 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 843 CCAGGCGCACCACTCCGCGAGCCACTACGACCCAGACGACGTCGGTGTATCCCGCTTAT 902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 TGACTAC-----GGCGCGGTGCGACGGCGCGCGGATCGCGACCTCCCGCGCTA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 903 CGAGACGAACCTTGACCCCTCTCGCTCGCATGCTGTGCTGGCAGCCGACACCGCGGG 962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 CAATGACACAGCCACCGGTGACCACTTCAACAGCAGCGCTGCGCAACCTCCACTCGGTGG 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 963 CTTGCAAGAGCGCTCAACCTCGGTTTAACTTCAACGGCACCAACTTCTTCATCAACAA 1022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 585 CTCCCTCGCGCTCGACGAGGACCTTTCTTCCCGTGGCGCTGGCGCTCTTCAACTG 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1023 CGCGA 1027
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 645 CTCCA 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
Bj270853 509 bp mRNA linear EST 09-APR-2002
LOCUS Bj270853 Y. Ogiwara unpublished cDNA library, Wh_oh Triticum
DEFINITION aestivum cDNA clone wh09022 5', mRNA sequence.
ACCESSION Bj270853.1 GI:20096494
VERSION Bj270853
KEYWORDS bread wheat.
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 509)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
JOURNAL Contact: Tadasu Shin-i
COMMENT Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..509
/organism="Triticum aestivum"

```

```
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh9022"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_oh"
/tissue_type="pistil at heading date"
/dev_stages="Feekes' scale 10.5"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
```

BASE COUNT 97 a 172 c 150 g 90 t

ORIGIN

```
Query Match 4.6%; Score 69; DB 13; Length 509;
Best Local Similarity 57.9%; Pred. No. 9.7e-05;
Matches 151; Conservative 0; Mismatches 95; Indels 15; Gaps 1;

Qy 78 GGTCAACGGCGTGTCCCTTCCCGCTCATCACCGGGAGAGAGACCGGCTCCAGCT 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 GTGAACGGCGAGTTCCCGGGCGGAGCTCACCGGAGGAGCGCGTGCAGCT 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 138 CAACGTCTGCACACTTGCACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGCA 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 CGCGTCTCAACACACAGCTGCGGCACACATGTC-----AATCCACTGGCA 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 198 CGGCTTCTTCCAGGAGGAGCACCACCTGCGCAGGAGCGCGTTCGTCAACAGTGCC 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CGGCATCGCGAGATGCGCAGCGGTGGCGGAGCGCGGCTAGTACGATGCGCC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 258 TATTCGTCGCGGCAATTCATTTCTAGTACACTTCCATGTCCCGACGAGGAGCAAGCTT 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 GATCAGAAGGGCCAGACCTAGTGTACAAGTTACCATCACCGGCGAGCGGCGCAGCT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 318 CTGGTACCACAGTCATCTGTC 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GTGGTGGCAGCGGCACATCTC 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 10
BJ279320
LOCUS BJ279320 Y. Ogihara unpublished cDNA library, wh_r Triticum
DEFINITION aestivum cDNA clone whr2g10 5', mRNA sequence.
ACCESSION BJ279320
VERSION BJ279320.1 GI:20101928
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 511)
AUTHORS Ogihara, Y. and Murali, K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
source 1. 511

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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whr2g10"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_r"
/tissue_type="root"
/dev_stages="Feekes' scale 1"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
```

BASE COUNT 90 a 181 c 150 g 90 t

ORIGIN

```
Query Match 4.6%; Score 69; DB 13; Length 511;
Best Local Similarity 53.7%; Pred. No. 9.7e-05;
Matches 197; Conservative 0; Mismatches 155; Indels 15; Gaps 2;

Qy 25 GTCGTGCGAGACCCCGCTCTCGCCGACGCGCTTCCTTCGGGATGCCATCGTGGTCAAC 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 GACATCTGTACAGTTAAAGTCCCGGACTGCTTCGAGAAGCTCGCCGTGACCGTCAAC 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 85 GCGCTGGTCCCTTCCTCCGCTCATCACCGGGAAGAAGGAGACCGCTTCAGCTCAACGTC 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 GCGGAGGCTCCCGGCGACCATTCGCGCCACGTTGGGTGA-----CACCATC 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 145 GTCGACACTTTCACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGCAGCGCTTC 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 ATCGTCCGCTCCATAACAAAGCTCGAGACCGAGAACACCGCCATCCACTGGCAGCGCATC 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 205 TTCCAGGAGGAGCAACACTGGGCGACGAGCCCGCTTCGTCAACCAAGTGCCTATTGCT 264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 308 CGCAGATCGACACCGCGTGGGCTGACGCGCTCGCGGCGTCCAGCAGTGCCTCATCTCTG 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 265 TCCGGGCAATTCATTCTGTACGACTTCCATGTGCCGACGAGGAGGAGTTCCTGGGTAC 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 CCGGGGAACCTTCACCTACAAATTC---GTCGTCGACAGGCGCTGGCAGTACCTGTAC 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 325 CACAGTCTCTCTTACGCAATACTGTGACGGCTCGGAGGACCGTTCGCTGCTAGCAG 384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 CATGCGCTACGGGATGACGCGCTGGCGGAGCTCAACGGCATGATGCTGGTCAACCGTG 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 385 CCCAAGG 391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 485 CCGGACG 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 11
BQ760633
LOCUS BQ760633
DEFINITION EBR003_SQ003_A18_R root, 3 week, waterlogged, cv Optic, EBR003
Hordeum vulgare cDNA clone EBR003_SQ003_A18 5', mRNA sequence.
ACCESSION BQ760633
VERSION BQ760633.1 GI:21969105
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 509)
AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
TITLE Development of Barley Transcriptome Resources

JOURNAL
COMMENT

Unpublished (2001)
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.

FEATURES
source

Location/Qualifiers
1. .509
/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBR003_SQ003_A18"
/clone_lib="root, 3 week, waterlogged, cv Optic, EBR003"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old waterlogged barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
Gene Function) project."
Gene Function 98 a 181 c 140 g 90 t

BASE COUNT
ORIGIN

Query Match 4.6%; Score 68.4; DB 14; Length 509;
Best Local Similarity 56.6%; Pred. No. 0.00013;
Matches 154; Conservative 0; Mismatches 106; Indels 12; Gaps 1;

QY 25 GTGTCGCGAAGCGCCCGCTGTCGCCGACGGCTTCCTTCGGGATGCCATCGTGGTCAAC 84
Db 208 GACATCTCGTACCAAGTAAAGTCCCGGACTGCTTCGAGAAGCTCGCGGTGACCGTCAAC 267
QY 85 GCGTGTGCTCTCCCGCTCATCACCGGAAGAGGAGACCGCTTCCAGCTCAAGTC 144
Db 268 GCGAGAGCTCCCGCGCGACATCCACGCGACGAGCGGA-----CACCATC 315
QY 145 GTCGACACCTTGACACACACAGCATCTCAAGTCCACTAGTATCCACTGGCAGGGTTC 204
Db 316 GTCGTGACGTCACACACAGCTCGACAGGAGACACCGCCATCCACTGGCAGGGATC 375
QY 205 TTCAGGACGACCAACTGGGACAGCGCCCGCTGCTCAACAGTGCCTATTGCT 264
Db 376 CGCGAGATTGACAGCGCTGGCGGCGAGCGGTGCGCGCGCTCAGCAGTGCCTTCCT 435
QY 265 TCCGGGATTCAATTCTGTAGCACTTCATGT 296
Db 436 CCGCGGAAACCTTCACCTACAAATTCGTCT 467

RESULT 12
BQ750959/c

LOCUS BQ750959 663 bp mRNA linear EST 18-JUL-2002
DEFINITION EST631522 DSCCT Colletotrichum trifolii cDNA clone pDSC1-67, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ750959
BQ750959.1 GI:21906364
EST.
Colletotrichum trifolii.
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 663)
Samad, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F., and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other ESTs: EST631523
Contact: Deborah A. Samad
Department of Plant Pathology

University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: WTSA677K More information is available at:
www.medicago.org
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).

FEATURES
source

Location/Qualifiers
1. .663
/organism="Colletotrichum trifolii"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC1-67"
/clone_lib="DSC1"
/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after
inoculation) grown in liquid culture (cutin minimal medium
containing 2%glucose)."
/lab_host="DH5alpha"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA. The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."
BASE COUNT 121 a 216 c 221 g 105 t

BASE COUNT
ORIGIN

Query Match 4.6%; Score 68.4; DB 14; Length 663;
Best Local Similarity 50.3%; Pred. No. 0.00014;
Matches 168; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1161 CGCCTTGGCCCGGGTCACGCGACCCCTTCCACCTGCACGGTCACGCTTCGCGGTCGT 1220
Db 645 CGGAAGCACCCTTCCACCTGCACGGCCACCATTTTCAGGTTCCTCCACCGCTCGGCCGA 586
QY 1221 TCGCAGCGCGGGAGCACCAGTATACACGACCCGATCTTCGCGACGTCGTGAG 1280
Db 585 GGACGCGCGGCTTCTCCGAGACCGGCTCGCCCTCCGCGGTACCCATCGCCGCGGA 526
QY 1281 CACGGGACGCCCGCGGGGCGACAGTCACGATCGCTTCCAGAGGACACCCCGG 1340
Db 525 CACCTCTGTCGAGGGCAACGGCAACTTCGTCTCCGCTTCGCGCGGACACCCCGG 466
QY 1341 GCGTGGTTCCTCCACTGCCACATCGACTTCCACCTGCACGGGCTTCGCGATCGTGT 1400
Db 465 CGTGTGGCTTTCACCTGCCACATCGAGTGGCAGATGACACAGGCTCTCGTCCACCAT 406
QY 1401 CGCAGAGCGTTTCGCGACGTGAAGCGGGGGAACCCGTTCCGAAGCGTGGTGGACCT 1460
Db 405 CGTCGAGGCGCCCGCGGCTGCGGGGGCTGCTGGCGTCCCGAGGACCACTGGAGGC 346
QY 1461 GTGCGCATCTACGACGGGTGACGAGGCTAAC 1494
Db 345 GTGCGCGCGGGGGGTCCCGACGAGGGCAAC 312

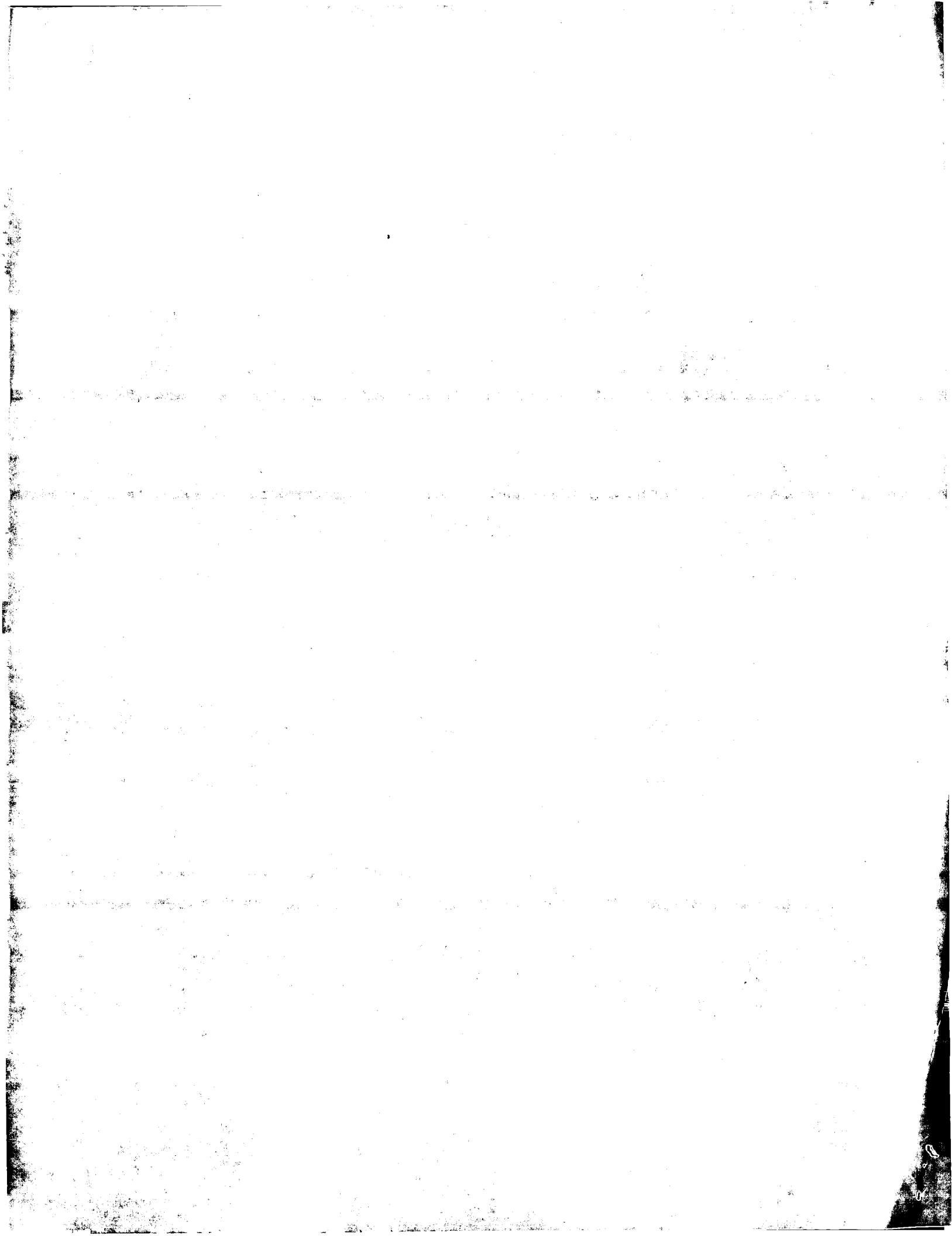
RESULT 13
AW671756

LOCUS AW671756 519 bp mRNA linear EST 19-JUL-2000
DEFINITION IGL_351_B05.b1_A002 Light Grown 1 (IG1) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION AW671756
VERSION AW671756.1 GI:7535653
KEYWORDS EST.
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor

Applicar

JOURNAL	Patent: WO 0196543-A 1 20-DEC-2001;
FEATURES	Prodigene, Inc. (US) : Genencor, Inc. (US)
source	Location/Qualifiers
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	RFPGLADATLNGRSPTAALAVLNQVGRYRFLVSIQDPNPTFSIDGHLN
	TVIEVDGINSPLVDSTQIFAAQSYFLVNAOTVGNVWRANPFTGVGFAGINS
	AILRYOGAPVAEPFTTQTSVPLIETLHPLARMPVPSPTPGVDKALNLAENG
	TNFFINNAFTFPTVPLVLSQALQSLGAOTADLLPAGSVYPLPAHSTIETLPATLAPG
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BASE COUNT	275 a 551 c 402 g 272 t
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Query Match	100.0%; Score 1500; DB 6; Length 1500;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1500; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCATCGGCGCGGTCGAGCCTCGTCGCGAAGCCCGCTCGCGCCGACGGCTTC 60
DB	1 GCATCGGCGCGGTCGAGCCTCGTCGCGAAGCCCGCTCGCGCCGACGGCTTC 60
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DB	61 CTTGCGGATGCATCGTGTCAACGGCTGTCCTTCCCGCTCATCACGGGGAAG 120
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DB	121 GGAGACCGCTTCCAGTCAACCTCGTCGACACCTTGACCAACACGATGCTCAAGTCC 180
QY	181 ACTAGTATCCACTGCGACGGCTTCTCCAGGACGACCACTGGGACAGGACCGCGG 240
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QY	241 TTCGTAACAGCTGCGCTATTCGTCGCGGCAATTCATTCGTACGACTTCATGTGCC 300
DB	241 TTCGTAACAGCTGCGCTATTCGTCGCGGCAATTCATTCGTACGACTTCATGTGCC 300
QY	301 GACGAGGAGGAGCTTGTGGTACACAGTCAATCTGTACGCAATATCTGTACGCGGCTG 360
DB	301 GACGAGGAGGAGCTTGTGGTACACAGTCAATCTGTACGCAATATCTGTACGCGGCTG 360
QY	361 CGAGGACGCTTGTGCTGTACGACCCCAAGGATCGGACGCGGCTACGATGTTGAC 420
DB	361 CGAGGACGCTTGTGCTGTACGACCCCAAGGATCGGACGCGGCTACGATGTTGAC 420
QY	421 AACGAGACGCGGTTCATCAGCTGTGACGCTGTACGACACCGCTGCGCGGCTCGGTC 480
DB	421 AACGAGACGCGGTTCATCAGCTGTGACGCTGTACGACACCGCTGCGCGGCTCGGTC 480
QY	481 AGGTTCCACTCGGCGGACCGCAGCTCAATCAATGTGTTGGCGGTGCGGCTCCACT 540
DB	481 AGGTTCCACTCGGCGGACCGCAGCTCAATCAATGTGTTGGCGGTGCGGCTCCACT 540
QY	541 CCCACCGCGGCTGCTGTGATCAACGCTCCAGGACGAAAGCGGTACCGTTCGCTGC 600
DB	541 CCCACCGCGGCTGCTGTGATCAACGCTCCAGGACGAAAGCGGTACCGTTCGCTGC 600
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DB	601 GTTTCGATCTCGTGAGCCCGCAACTACAGCTTACAGCTGACGCGGACAACTGACGCTC 660

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QY	781	CGAACCCGAACTTCGGAACGTTGGGTTCCGCGGGGGATCAACTCGCCATCTCGCC	840
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QY	841	TACCAAGCGCACCACTCGCGAGCCCACTAGGACCCAGACGCTCGGTGATCCCGTT	900
Db	841	TACCAAGCGCACCACTCGCGAGCCCACTAGGACCCAGACGCTCGGTGATCCCGTT	900
QY	901	ATCAGAGCAACTTGCACCCCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCGG	960
Db	901	ATCAGAGCAACTTGCACCCCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCGG	960
QY	961	GGGTCGACAAAGGGCTCAACTCGCGTTAACTTCAACGACCAACTTCTTCAATCAAC	1020
Db	961	GGGTCGACAAAGGGCTCAACTCGCGTTAACTTCAACGACCAACTTCTTCAATCAAC	1020
QY	1021	AACGCGACTTTCAGCGCGCGACCGTCCCGTACTCTCCAGATCTGAGCGGTGCGCAG	1080
Db	1021	AACGCGACTTTCAGCGCGCGACCGTCCCGTACTCTCCAGATCTGAGCGGTGCGCAG	1080
QY	1081	ACCACACAAGCCTGCTCCCTGCGAGGCTCTGTACCCGCTTCCCGGCGCACTCCACCATC	1140
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QY	1261	ATCTTCGCGAGCTGCGAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1320
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QY	1321	TTCAGAGGAGCAACCGCGCGCGCTGCTTCCCTCCACTGCGACATCGACTTCCACTCGAC	1380
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QY	1381	CGGCGCTTCGCGATCGTGTTCGAGAGAGCGTTGCGGACGTTGAAGGGGGAACCCGGTT	1440
Db	1381	CGGCGCTTCGCGATCGTGTTCGAGAGAGCGTTGCGGACGTTGAAGGGGGAACCCGGTT	1440
QY	1441	CGAAGGCGTGTGCGGACCTGCGCGATCTACAGCGGCTGAGCGAGGCTTAACAGTGA	1500
Db	1441	CGAAGGCGTGTGCGGACCTGCGCGATCTACAGCGGCTGAGCGAGGCTTAACAGTGA	1500
RESULT 2			
TVU44430			
LOCUS	TVU44430	1932 bp	mRNA linear PLN 17-APR-2001
DEFINITION	Trametes versicolor laccase I (lcc1) mRNA, complete cds.		
ACCESSION	U44430		
VERSION	U44430.1	GI:1172162	
KEYWORDS			
SOURCE	Trametes versicolor.		
ORGANISM	Trametes versicolor		
REFERENCE	1 (bases 1 to 1932)		
AUTHORS	Ogawa, E., Pollock, W.B. and Smith, M.		
TITLE	Cloning and sequence analysis of two laccase complementary DNAs		
JOURNAL	from the ligninolytic basidiomycete Trametes versicolor		
MEDLINE	Gene 196 (1-2), 113-119 (1997)		
	97464057		



9322748

PUBMED

2 (bases 1 to 1932)
REFERENCE
Ong, E., Pollock, B. and Smith, M.
AUTHORS
Direct Submission
TITLE
Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of
JOURNAL
British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T
123, Canada

FEATURES
source

Location/Qualifiers
1. 1932
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/strain="52J"
/db_xref="taxon:5325"
1. 1932
/gene="lccI"
184. 1743
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/note="phenol oxidase"
/codon_start=1
/product="laccase I"
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/translation="MGLQSFVTLALVARSLLAIGPVASLVVANAPSPDGLRDA
IVNVVPSPLITGKGRDLNVDLTHNSMLKSTSIHWHGFFQAGTNWADGPAFV
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NESTVITLDMYHTAARLGRPLGADATLNGIRGASSTPTAALAVINVQHGKRYRF
RLVNSICDPNTYSIDGHNLTVEVDGINSOPLVDLSIOIFAAORYSEVLNANQTVGN
YWRANPNFTGVSFAGGINSAILRYOGAPVAEPITTOFTSVIPLIENLPLARMVPV
GSPTPGVDKALNLFNFTGPNFNNATFTPTVYVLLQILSGAQDQLLPAQSVY
PLAHSIETLPTALAPGAPPHFHGHAFVRSAGSTVYNDPIFRDYYVSTGT
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FYDGLSEANO"

gene

CDS

BASE COUNT
ORIGIN

367 a 665 c 521 g 379 t

Query Match 100.0%; Score 1500; DB 8; Length 1932;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCATCGGGCGGGTGGGAGCTCGTCTCGCAAGCCCGCTCTCCCGGACGGCTTC 60
Db 244 GCCATCGGGCGGGTGGGAGCTCGTCTCGCAAGCCCGCTCTCCCGGACGGCTTC 303
Qy 61 CTTGGGATGCCATCGTGGTCAAGGGGTGTCTCCCTCCCGCTCATCACGGGAAGA 120
Db 304 CTTGGGATGCCATCGTGGTCAAGGGGTGTCTCCCTCCCGCTCATCACGGGAAGA 363
Qy 121 GGAGACCGCTTCCAGCTCAAGCTGTGACACCTTGACCAACACACGATGCTCAAGTCC 180
Db 364 GGAGACCGCTTCCAGCTCAAGCTGTGACACCTTGACCAACACACGATGCTCAAGTCC 423
Qy 181 ACTAGTATCCACTGGCAGCGCTTCTCCAGGACGACCAACTGGGAGACGGACCGCG 240
Db 424 ACTAGTATCCACTGGCAGCGCTTCTCCAGGACGACCAACTGGGAGACGGACCGCG 483
Qy 241 TTCCTCAACAGTCCCTATGCTTCCGGGCAATTCATTCGTACGACTTCCATGTGCC 300
Db 484 TTCCTCAACAGTCCCTATGCTTCCGGGCAATTCATTCGTACGACTTCCATGTGCC 543
Qy 301 GACCAGGACGGAAGCTTCTGTGTACACAGTCATCTGTCTAGCAATATCTGTAGCGGCTG 360
Db 544 GACCAGGACGGAAGCTTCTGTGTACACAGTCATCTGTCTAGCAATATCTGTAGCGGCTG 603
Qy 361 CGAGGACCGTTCGTGTGTACGACCCCAAGATCCGACGCCGACCGCTACGATGTTGAC 420
Db 604 CGAGGACCGTTCGTGTGTACGACCCCAAGATCCGACGCCGACCGCTACGATGTTGAC 663
Qy 421 AACGAGACGACGTCATCAGCTTGACCGACTGGTACACACCGCTGCCCGGCTGGTCCC 480
Db 564 AACGAGACGACGTCATCAGCTTGACCGACTGGTACACACCGCTGCCCGGCTGGTCCC 723
Qy 481 AGGTTCCTCACTCGCGGGACGACCGCTCATCAATGCTCTGGGGGTGGGCTCCACT 540

RESULT 3

AY049725

LOCUS

DEFINITION

AY049725

ACCESSION

VERSION

AY049725

Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.

AY049725

AY049725.1 GI:15617226

2408 bp mRNA linear PLN 13-SEP-2001

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:12:08 ; Search time 3053 Seconds
(without alignments)
14298.791 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gcatcgccggtggtgag.....tgacggaggctaaccagtga 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
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- 27: em_un.*
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- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1500	100.0	1500	6	AX384796	AX384796 Sequence
2	1500	100.0	1932	8	TVU44430	U4430 Trametes ve
3	483	32.2	2408	8	AY049725	AY049725 Trametes
4	287	19.1	2127	8	TVU44851	U44851 Trametes ve
5	246	16.4	2689	8	TMTLCCB	L49377 Trametes vi
6	246	16.4	2880	6	I65230	I65230 Sequence 3
7	158	10.5	7986	6	AX015224	AX015224 Sequence
8	59	3.9	2700	8	PGU65399	U65399 Basidiomyc
9	41	2.7	1829	8	AF176230	AF176230 Polyporus
10	38	2.5	1563	8	AF414109	AF414109 Trametes
11	38	2.5	1739	3	AB006824	AB006824 Trachyder
12	38	2.5	1869	8	AF491759	AF491759 Basidiomy
13	38	2.5	2020	8	AF176231	AF176231 Polyporus
14	38	2.5	2043	8	AF388910	AF388910 White-rot
15	38	2.5	2417	8	TMTLCCA	L49376 Trametes vi
16	38	2.5	2418	6	I65229	I65229 Sequence 1
17	38	2.5	2780	8	BLACCASEG	Z12156 Basidiomyc
18	38	2.5	2800	8	AF162785	AF162785 Basidiomy
19	38	2.5	3963	8	AY081188	AY081188 Trametes
20	38	2.5	5762	6	AX015225	AX015225 Sequence
21	35	2.3	1497	6	E02225	E02225 CDNA encodi
22	35	2.3	1497	6	E02226	E02226 CDNA encodi
23	35	2.3	1618	6	E02617	E02617 DNA encodin
24	35	2.3	1618	6	E02618	E02618 DNA encodin
25	35	2.3	1618	6	E02624	E02624 DNA sequenc
26	35	2.3	1618	6	E02625	E02625 DNA sequenc
27	35	2.3	2049	6	E02224	E02224 gDNA encodi
28	35	2.3	2700	8	PGU65401	U65401 Basidiomyc
29	35	2.3	2812	8	TMTLCCB	L49376 Trametes vi
30	35	2.3	2904	8	CRILIPHE	M60560 C.hirsutus
31	35	2.3	2907	8	CRILIPHA	M60561 C.hirsutus
32	35	2.3	2925	6	I65233	I65233 Sequence 9
33	35	2.3	3099	8	D84235	D84235 Coriolus ve
34	35	2.3	4996	8	AF414807	AF414807 Trametes
35	33	2.2	1572	6	AX002145	AX002145 Sequence
36	33	2.2	1572	6	AX002146	AX002146 Sequence
37	33	2.2	3284	6	AX002152	AX002152 Sequence
38	32	2.1	1584	8	AF185275	AF185275 Ganoderma
39	32	2.1	2400	8	PGU65400	U65400 Basidiomyc
40	30	2.0	1557	8	AF152170	AF152170 Pycnoporu
41	30	2.0	2629	8	AF025481	AF025481 Pycnoporu
42	30	2.0	2684	8	D13372	D13372 Coriolus ve
43	30	2.0	2800	8	TVLCC1	X84683 T.versicolo
44	30	2.0	2860	6	I65232	I65232 Sequence 7
45	30	2.0	2906	8	TMTLCCD	L78077 Trametes vi

ALIGNMENTS

RESULT 1	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
LOCUS	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
DEFINITION	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
ACCESSION	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
VERSION	AX384796.1	GI:19577931	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
KEYWORDS	AX384796.1	GI:19577931	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
SOURCE	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
ORGANISM	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
REFERENCE	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
AUTHORS	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
TITLE	AX384796	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002

JOURNAL Patent: WO 0196543-A 1 20-DEC-2001;
Prodigene, Inc. (US) ; Genencor, Inc. (US)
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LOCUS
DEFINITION
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ACCESSION
U44430
VERSION
U44430.1
GI:1172162
KEYWORDS
SOURCE
Trametes versicolor.
ORGANISM
Trametes versicolor.
REFERENCE
1 (bases 1 to 1932)
AUTHORS
Ong, E., Pollock, W.B. and Smith, M.
TITLE
Cloning and sequence analysis of two laccase complementary DNAs
from the ligninolytic basidiomycete Trametes versicolor
JOURNAL
Gene 196 (1-2), 113-119 (1997)
MEDLINE
97464057

PUBMED 9322748
REFERENCE 2 (bases 1 to 1932)
AUTHORS Ong E., Pollock, B. and Smith, M.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T 1Z3, Canada

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BASE COUNT 367 a 521 g 379 t
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AY049725
LOCUS
DEFINITION
ACCESSION
VERSION

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Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.
AY049725
AY049725.1 GI:15617226

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ACCESSION I65230
VERSION I65230.1 GI:2481800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2880)
AUTHORS Yaver,D.Sue., Xu,F., Dalb.o slashed.ge,H., Schneider,P. and Aaslyng,D.A.
TITLE Dye compositions containing purified polyporus laccases and nucleic acids encoding same
JOURNAL Patent: US 5667531-A 3 16-SEP-1997;
FEATURES Location/Qualifiers
BASE COUNT 547 a 908 c 793 g 632 t
ORIGIN
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ACCESSION AX015224
VERSION AX015224.1 GI:10041257
KEYWORDS
SOURCE Trametes versicolor.
ORGANISM Trametes versicolor.
REFERENCE 1 (bases 1 to 7986)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphylliphorales; Trametes.

AUTHORS Pfaller,R., Van Den Hondel,C., Van Gorcom,R. and Hensing,J.
TITLE Expression system for producing proteins
JOURNAL Patent: WO 9951757-A 1 14-OCT-1999;
PFALLER RUPERT (DE); CONSORTIUM ELEKTROCHEM IND (DE); DEN HONDEL CORNELIS VAN (NL); GORCOM ROBERTUS VAN (NL); HESSING JOHANNA (NL)
FEATURES Location/Qualifiers
BASE COUNT 1698 a 2404 c 2107 g 1777 t
ORIGIN
Query Match 10.5%; Score 158; DB 6; Length 7986;
Best Local Similarity 100.0%; Pred. No. 7.7e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 584 GCTACCGCTTCGTCGTTTCGATCTCGTGCAGCCGGAACCTACAGCTTCAGCATCGACG 643
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Db 2170 GCTACCGCTTCGTCGTTTCGATCTCGTGCAGCCGGAACCTACAGCTTCAGCATCGACG 2229
|||||
QY 644 GGCACAATCTGACCGTCATCGAGTGCAGGTATCAACAGCCAGCCTCTCTTGTGACT 703
|||||
Db 2230 GGCACAATCTGACCGTCATCGAGTGCAGGTATCAACAGCCAGCCTCTCTTGTGACT 2289
|||||
QY 704 CTATCCAGATCTTCGGCGCGCAGCGCTACTCTTGTG 741
|||||
Db 2290 CTATCCAGATCTTCGGCGCGCAGCGCTACTCTTGTG 2327
|||||
RESULT 8
PGU65399
LOCUS PGU65399 2700 bp DNA linear PLN 19-JUL-1997
DEFINITION Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.
ACCESSION U65399
VERSION U65399.1 GI:2264395
KEYWORDS basidiomycete CECT 20197.
SOURCE basidiomycete CECT 20197
ORGANISM Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphylliphorales; Polyporaceae.
REFERENCE 1 (bases 1 to 2700)
AUTHORS Mansour,M., Suarez,T., Fernandez-Larrea,J.B., Brizuela,M.A. and Gonzalez,A.B.
TITLE Identification of a laccase gene family in the new lignin-degrading basidiomycete CECT 20197
JOURNAL Appl. Environ. Microbiol. 63 (7), 2637-2646 (1997)
MEDLINE 97355933
PUBMED 9212414
REFERENCE 2 (bases 1 to 2700)
AUTHORS Mansour,M.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1996), Molecular Microbiology, Biological Research Center (CIB), Consejo Superior de Investigaciones Cientificas, Velazquez 144, Madrid 28006, Spain
FEATURES Location/Qualifiers
BASE COUNT 1. .2700
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/strain="CECT 20197"
/db_xref="taxon:51095"
301..2369
/gene="pox1"
join(301..480,534..602,656..776,839..952,1006..1069,
1125..1220,1280..1436,1494..1691,1756..2019,2073..2369)
/gene="pox1"
/EC_number="1.10.3.2"
/note="laccase; blue-copper oxidase"
/codon_start=1
/product="phenoloxidase"
/protein_id="AAB63443.1"
/db_xref="GI:2264396"
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VVYGVFPPGLITGKKQDFQLNIDLTNHTMLKSTSIHWGFFQAGTWNADGPVY
NQCPISGTGHAFLYDFHVPDQAGTFWYHSHLSLTQYCDGLRGPIVYVDPDLPATRYDVD

DESTVITLSDMYHTAATLGLSGRLGADATLNLGLRSSSTPTANTVTINVOHKRYRE
RLVLSLSDPNHTFSDGHNLFVIEVDGNSKPLTVDSIQIFRAQKYSFVLNANQVGN
YWRANPNFGTFRAGGINSALLRQAGPIETPTVQTSIVPLVETNLHPLPPIVP
GLPVSQGVDAKLNLFNGFNFFINNATFPTPTVPLVLLQLLSGASTQDILLPPGSYV
PLPASHSEITLPAFTLAPGAPPHLGHVFAVRSSTAYNVDIFRDVYSTG
PAAGDNVTIRFHTDNPFGFWFLHCHIDFLEAGFAIVFAEDVADVKRAANPVPKAWSDLC
PTYDALAESGDL"

BASE COUNT 573 a 834 c 672 g 621 t

Query Match 3.9%; Score 59; DB 8; Length 2700;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 CACTGGCAGCGTCTTCAGGAGGACACCACTGGGAGAGGACCGCGTTCGTCAA 248
|||||
Db 656 CACTGGCAGCGTCTTCAGGAGGACACCACTGGGAGAGGACCGCGTTCGTCAA 714
|||||

RESULT 9
AF176230 1829 bp mRNA linear PLN 01-SEP-2000
LOCUS
DEFINITION Polyporus ciliatus laccase (lcc3-1) mRNA, complete cds.
ACCESSION AF176230
VERSION AF176230.1 GI:9957142
KEYWORDS
SOURCE Polyporus ciliatus.
ORGANISM Polyporus ciliatus.

REFERENCE
AUTHORS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
TITLE Aphyllophorales; Polyporaceae; Polyporus.
JOURNAL 1. (bases 1 to 1829)
REFERENCE 2 (bases 1 to 1829)
AUTHORS Schnee.C. and Eggert.C.
TITLE Isolation and characterization of three laccase genes from the
white-rot fungus Polyporus ciliatus and their expression during
fruiting
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1829)
AUTHORS Schnee.C. and Eggert.C.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Institute of General Microbiology and
Microbial Genetics, Friedrich-Schiller University Jena, Neugasse
24, Jena

FEATURES
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1..1829
Location/Qualifiers
/organism="Polyporus ciliatus"
/strain="Th1"
/db_xref="taxon:134555"
/tissue_type="vegetative mycelia"
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1..1829
/gene="lcc3-1"
CDS
72..1628
/gene="lcc3-1"
/EC_number="1.10.3.1"
/note="p-phenol oxidase"
/codon_start=1
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/protein_id="AAG09229.1"
/db_xref="GI:9957143"

/translation="MARFSLLSFVTLFVSAAYAAIGVTDLTVDANIISPDGFENRA
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DDSDVITLADWYHVAALGKLPREPSSDSNLINGLGRSPSTADLAVISYTGKRYR
PRLVSLSDPNYTESIDGHQTLVTEADGISIQPVGDSIQIFAAQRISFVLTAQDPV
DNWVRANPNFGNTGFAFGINSAILRVDGAIEPTTQNTGNLLELLELHLPFTTPV
PGNPTQGGAGDNLNIAFNFGTDFSIINGATFTPPSPVLLQIIISGANSQDILLPSGSV
YALPNSNIEITFATAAAGAPGPHFLHGHAFVAVRSAGSTVYNDPNVYRDVYSTG
TPGDNVTIRFOTDNPFGFWFLHCHIDFLEAGFAIVFAEDIPDVASANPVPQAWFDLCP
IYNALDPSDQ"

BASE COUNT 349 a 622 c 427 g 431 t

Query Match 2.7%; Score 41; DB 8; Length 1829;
Best Local Similarity 100.0%; Pred. No. 1e-09;

MATCHES 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGAGCG 1382
|||||
Db 1470 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGAGCG 1510
|||||

RESULT 10
AF414109 1563 bp mRNA linear PLN 26-SEP-2001
LOCUS
DEFINITION Trametes versicolor laccase B precursor (lacc1) mRNA, complete cds.
ACCESSION AF414109
VERSION AF414109.1 GI:15778441
KEYWORDS
SOURCE Trametes versicolor.
ORGANISM Trametes versicolor.

REFERENCE
AUTHORS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
TITLE Aphyllophorales; Trametes.
JOURNAL 1 (bases 1 to 1563)
REFERENCE 2 (bases 1 to 1563)
AUTHORS Jolivald,C., Madzak,C., Caminade,E. and Mouglin,C.
TITLE 2,5-xyllidine induced laccase from the basidiomycete Trametes
versicolor ATCC 32745
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Jolivald,C., Madzak,C., Caminade,E. and Mouglin,C.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2001) unite de Phytopharmacie, INRA, Route de
Saint Cyr, Versailles 78026, France

FEATURES
source
1..1563
Location/Qualifiers
/organism="Trametes versicolor"
/strain="ATCC 32745"
/db_xref="ATCC:32745"
/db_xref="taxon:5325"
gene
1..1563
/gene="lacc1"
CDS
1..1563
/gene="lacc1"
/EC_number="1.10.3.2"
/note="oxidoreductase; Induced by 2,5-xyllidine"
/codon_start=1
/product="laccase B precursor"
/protein_id="AAL07440.1"
/db_xref="GI:15778442"

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DNDTIVITLADWYHVAALGKLPAPPLGADATLINGKRSPTTADLSVITSPGKRYR
PRLVSLSDPNYTESIDGHNTIETDSINTAPLVYDSIQIFAAQRISFVLTAQDPV
NWTNRANPNFGVGTGGINSAILRVDGAIEPTTQNTSTAPLNEVNLHPLVATAV
PGSPVAGGVDAKLNLFNGFNFFINNATFPTPTVPLVLLQLLSGASTQDILLPPGSV
YSLPSNADIEISFPATAAAGAPGPHFLHGHAFVAVRSAGSTVYNDPNVYRDVYSTG
TPAAGDNVTIRFOTDNPFGFWFLHCHIDFLEAGFAIVFAEDIPDVASANPVPQAWSDLC
CPTYDARDPSDQ"

sig_peptide 1..63
BASE COUNT 273 a 591 c 387 g 309 t 3 others
ORIGIN

Query Match 2.5%; Score 38; DB 8; Length 1563;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 1405 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1442
|||||

RESULT 11
AB006824 1739 bp mRNA linear INV 03-JUN-1998
LOCUS
DEFINITION Trachyderma tsunodae mRNA for Billrubin Oxidase, complete cds.
ACCESSION AB006824

```

VERSION AB006824.1 GI:3176127
SOURCE Bilirubin Oxidase.
ORGANISM Trachyderma tsunodae (strain:K-2593) cDNA to mRNA.

REFERENCE
AUTHORS Iwamoto,H., Watanabe,H., Minakami,M., Hirose,J., Hiromi,K.,
Mukai,H., Yoshioke,H. and Kato,I.
TITLE Purification, Characterization, and Molecular Cloning of Bilirubin
Oxidase from Trachyderma tsunodae K-2593
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1739)
AUTHORS Iwamoto H.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1997) Hiroyuki Iwamoto, Fukuyama University,
Faculty of Engineering, Gakuen-cho, Fukuyama, Hiroshima 729-02,
Japan (E-mail:iwamoto@fubac.fukuyama-u.ac.jp, Tel:0849-36-2111,
Fax:0849-36-2023)
FEATURES
source Location/Qualifiers
1..1739
/organism="Trachyderma tsunodae"
/strain="K-2593"
/db_xref="taxon:65050"
13..1578
/codon_start=1
/product="Bilirubin Oxidase"
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/db_xref="GI:3176128"
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AIYVNGVFAPLITGKGRFQNLNIDNMTNMLKSTSIHHGFFQKGTNMADGGAF
VNOCPAPGHSFLYDFRPDQAGTFWVHSLSTQYCDGLRGPVIVYDQDPHKSLYDV
DNDSTVITLADWVHAARLGPRLGASLTVINGLGRSLSTPNADLAVISVTOGKRYR
FRLLISCDPFHFSIDGHLTIIEADSVNTEPLVDVPIFAGQKYSFVLSAVKDIID
NYWIRADPGFTTGAGINSAILRDYGAAPIETAVLAPVSNPLVETDLHLEMDP
VQGRPTKGGYKAINLDIFSFEFNFINNATFTSPVPIILQIMSGAQAQDLPLPSGS
VIELPAQSTIELLPATVNAAGVPVPHFHLHGHTFAVVRSGASTAYNDNPIMRDVYST
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evidence=experimental
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BASE COUNT 351 a 587 c 416 g 385 t
ORIGIN
Query Match 2.5%; Score 38; DB 3; Length 1739;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 1420 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1457

RESULT 12
AF491759 AF491759 1869 bp mRNA linear PLN 09-APR-2002
LOCUS Basidiomycete C30 lacase 1 (lac1) mRNA, complete cds.
DEFINITION Basidiomycete C30 lacase 1 (lac1) mRNA, complete cds.
ACCESSION AF491759
VERSION AF491759.1 GI:20086990
KEYWORDS basidiomycete C30.
SOURCE basidiomycete C30.
ORGANISM basidiomycete C30
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; unclassified Coriolaceae.
REFERENCE 1 (bases 1 to 1869)
AUTHORS Klonowska,A. and Tron,T.
TITLE clac1, the cDNA encoding the LAC1 from the basidiomycete C30
JOURNAL Unpublished

REFERENCE
AUTHORS Klonowska,A. and Tron,T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2002) Chemistry, LBS UMR 6517 CNRS, Avenue
Escadrille Normandie-Niemen, Marseille 13397, France
FEATURES
source Location/Qualifiers
1..1869
/organism="basidiomycete C30"
/isolate="C30"
/db_xref="taxon:191221"
1..1869
/gene="lac1"
1..41
/gene="lac1"
42..1595
/gene="lac1"
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/EC_number="1.10.3.2"
/feature="LAC1; polyphenoloxidase; similar lac1 of GenBank
Accession Number AF162785"
/codon_start=1
/product="laccase 1"
/protein_id="AAM10738.1"
/db_xref="GI:20086991"
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AILVNDVFPSPPLITGNKGRFQNLNIDNMTNMLKSTSIHHGFFQKGTNMADGGAF
VNOCPSTGHAFYLDQVPDQAGTFWVHSLSTQYCDGLRGPVIVYDQDPHKSLYDV
DDSTVITLADWVHAARLGPRLGASLTVINGLGRSLSTPNADLAVISVTOGKRYR
RLVSLCDPNHTFSIDGHSLSLTVIEADSVNLKPTQVDSIQIFAAQRYSFVLNADQVDN
YNIRALPNSCTRNFGDVNSAILRDYGAAVPEVTTQTPTSTQPLVSAULTTLRGTAA
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SPANADIETSLPATSAAGFPFPHFHLHGHTFAVVRSGASTITNANPVTRDVSSTGS
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1596..1869
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/gene="lac1"
polyA_site 1841
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BASE COUNT 364 a 631 c 466 g 408 t
ORIGIN
Query Match 2.5%; Score 38; DB 8; Length 1869;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 1437 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1474

RESULT 13
AF176231 AF176231 2020 bp mRNA linear PLN 01-SEP-2000
LOCUS Polyporus ciliatus lacase (lcc3-2) mRNA, complete cds.
DEFINITION Polyporus ciliatus lacase (lcc3-2) mRNA, complete cds.
ACCESSION AF176231
VERSION AF176231.1 GI:9957144
KEYWORDS Polyporus ciliatus.
SOURCE Polyporus ciliatus.
ORGANISM Polyporus ciliatus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Polyporaceae; Polyporus.
REFERENCE 1 (bases 1 to 2020)
AUTHORS Schnee,C. and Eggert,C.
TITLE Isolation and characterization of three laccase genes from the
white-rot fungus Polyporus ciliatus and their expression during
fruiting
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2020)
AUTHORS Schnee,C. and Eggert,C.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Institute of General Microbiology and
Microbial Genetics, Friedrich-Schiller University Jena, Neugasse

```



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24, Jena 07743, Germany
Location/Qualifiers
1..2020
/organism="Polyporus ciliatus"
/strain="Th1"
/db_xref="taxon:134555"
1..2020
/gene="lcc3-2"
71..1645
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/protein_id="AAG09230.1"
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DVEDSTVITLADMTHTAARLGPFCPLGSDSTLNLGRFAGGADADPLTVISVTSKG
RYRFLRISGDPNFTFTIOGHTMTVIEVDVNVQYEVSDSIQIFAGORYSEVLTDGQ
AVDNYWIOAIPISGITTDDGWSAILRDVGDADIVEPAAVTSNPLAVERSLVPLEN
LAAPEPTIGVDGVDPLNLDSEFDTNFAINGATFTPTVPVLLQMSGAQDVADLLPS
GSIVSLPNATIELSFPLTANAGAPHPFHLHGHTFFVVRSGASTENYNVNPQORDT
VSTGAGDNVTIRFTTNNPGMPWFLHCHIDFLEAGFAVVFGEIDIPSIDANPPSSAWE
DLCPYNSVYPNGDN"
BASE COUNT      389 a 712 c 468 g 451 t
ORIGIN

Query Match      2.5%; Score 38; DB 8; Length 2020;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 1481 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1518

RESULT 14
AF388910
LOCUS      White-rot fungus AH28-2 laccase gene, partial sequence.
DEFINITION
ACCESSION  AF388910
VERSION    AF388910.1 GI:14669597
KEYWORDS   white-rot fungus AH28-2.
SOURCE     white-rot fungus AH28-2.
ORGANISM   Eukaryota; Fungi; Basidiomycota.
REFERENCE  1 (bases 1 to 2043)
AUTHORS    Xiao,Y., Wu,J. and Shi,Y.
TITLE      Cloning of laccase gene from a new white-rot fungus AH28-2
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 2043)
AUTHORS    Xiao,Y., Shi,Y., Chen,Q., Wang,J., Hang,J., Wu,J., Wang,Y., Jia,R.
            and Zhang,M.
TITLE      Direct Submision
JOURNAL    Submitted (02-JUN-2001) School of Life Science, Anhui University, 3
            Feixi Road, Hefei, Anhui 230039, P.R. China
FEATURES
Source
1..2043
/organism="white-rot fungus AH28-2"
/strain="AH28-2"
/db_xref="taxon:164952"
/note="a newly isolated strain, effectively produces
laccase by induction when grown on a synthetic medium"
<1..>2043
/gene="laccase"
/note="coding region not determined"
BASE COUNT      403 a 669 c 506 g 465 t
ORIGIN

Query Match      2.5%; Score 38; DB 8; Length 2043;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
Db 1888 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1925

RESULT 15
TMTLCCA
LOCUS      Trametes villosa (clone LCC1) laccase gene, exons 1-9, complete
DEFINITION
ACCESSION  L49376
VERSION    L49376.1 GI:1100243
KEYWORDS   laccase.
SOURCE     Trametes villosa
ORGANISM   Trametes villosa
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Aphyllophorales; Trametes.
REFERENCE  1 (bases 1 to 2417)
AUTHORS    Yaver,D.S., Xu,F., Golightly,E.J., Brown,K.M., Brown,S.H.,
            Rey,M.W., Schneider,P., Halkier,T., Mondorf,K. and Dalbooge,H.
TITLE      Purification, characterization, molecular cloning, and expression
            of two laccase genes from the white rot basidiomycete Trametes
            villosa
JOURNAL    Appl. Environ. Microbiol. 62 (3), 834-841 (1996)
MEDLINE    97076915
PUBMED     8975623
FEATURES
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1..2417
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/db_xref="taxon:47662"
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/tissue_type="mycelia"
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1050..1145,1197..1353,1411..1608,1663..2223)
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FRVLSLQDPNVTESIDGHNMTLETDSINTAPLVDSIQIFAQRYSEVLEAQAQVD
NWTARNFNGVGTGGINSAIRLDGAAAVEPTTOTTITAPLNEVNLHPLPVTAV
PGSPVAGVDIAINMAFNFTNGTFFNGTFTPTPTPVLLQIISGAQAQDLPLPSGV
YSLPSNADIEISFATAAPGAPHPFHLHGHTFFVVRSGASTENYNVNPQORDT
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464..532
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/number=3
710..764
intron
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